gallus gall clostridium homo sapien

095153 001397 0001397 000496 0008378 014149 P39285 P48673

neurospora

escherichia carassius a

homo sapien

432 AA.

homo sapien

mus musculu canis famil

human papil

cyprinus ca

OM protein

Run on:

Sequence:

Searched:

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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUB-CYTOTOXIC T-CELL;
MEDLINE-R115527. Puhwd=1550794;
KOyama T., Hall L.R., Haser W.G., Tonegawa S., Saito H.;
"Structure of a cytotoxic T-lymphocyte specific gene shows a strong homology to fibrinogen beta and gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Association of mouse fibrinogen-like protein with murine hepatitis; virus-induced prothrombinase activity."; J. Virol. 69:5033-5038(1995).
-i. FUNCTION: CONVERTS PROTHROMBIN TO THROWBIN.
-i. TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS VIRUS STRAIN 3 (MIN'-3).
-!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                      01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROTHROMBINASE PRECURSOR (FIBRINOGEN-LIKE PROTEIN) (CYTOTOXIC T-LYMPHOCYTE SPECIFIC PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRANT=BALB/CJ; TISSUE=PERITONEAL MACROPHAGE;
MEDILINE=953333285; Pubbed=7609073;
Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,
                                                                                                                                                                      ALIGNMENTS
             VL1_HPV37
LMG1_MOUSE
                                               DYNA_NEUCR
MYSE_CHICK
BXE_CLOBO
                                                                                              Y136_HUMAN
YJEP_ECOLI
VIMB_CARAU
                                    BRC1_CANFA
                                                                                  G160_HUMAN
                                                                                                                                   UTRO_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M16238; AAA37624.1; -.
EBBL; M15761; AAA37624.1; JOINED.
EMBL; S78773; AAB34823.1; -.
PIR; A27447; A27447.
455
507
1607
1878
1300
1250
579
950
11107
450
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
44444444444
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                                                                                                                                                                                                                               FIBX_MOUSE
P12804;
104.5
104.5
104.5
102.5
101.5
101.5
100.5
100.5
100.5
100.5
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(without alignments)
723.227 Million cell updates/sec
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homo sapien
sus scrofa
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homo sapien
petromyzon
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homo sapien
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gallus gall
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                                                                                                                                           2340
1 MRLPGWLWLSSAVLAACRAV......GYKSSFKQAKMMIRPKNFKP 432
                                                                                 February 27, 2001, 12:52:02; Search time 19.29 Seconds
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P21520 |
P55918 |
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                          hits satisfying chosen parameters:
                                                                                                                                                                                                                   88757 seqs, 32294092 residues
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FIBG_HUMAN
FIBH_HUMAN
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FIBA_RAT
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FIBG_PETMA
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MMGL_MOUSE
MYSS_HUMAN
MYSE_HUMAN
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FIBA_PARPA
FIBB_HUMAN
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SCA_DROME
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Maximum Match 100%
Listing first 45 summaries
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TENA_CHICK
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    protein search, using sw model

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FIBG_RAT
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Gapop 10.0 , Gapext 0.5
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426.5
426.5
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416.5
414.5
408.5
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377
372.5
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Database :

Result Š. HSSP; P02671; IFZD.
MGD; MGI:103266; FGL2.
INTERPRO; IPR002181; PFAM; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
T-cell; Cytolysis; Blood coagulation; Signal.

mus musculu homo sapien homo sapien schizosacch

P49300 P12882 P11055 P47460

bos taurus

rattus norv tetrahymena gallus gall

Q10411 P12847

HMW2_MYCGE YD86_SCHPO MYSE_RAT

110 110 109.5 108 106.5 106.5

MYS_PODCA TE95_TETTH

MYSC_CHICK

mycoplasma

podocoryne

Q05000 Q94819 P29616

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cleavage site.";
Biochemistry 30:3290-3294(1991).
-i- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANEOUS: CONVERSION OF FIBRINGGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                       Gaps
                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
MEDLINE-91182745; PubMed-2009266;
Weissbach L., Oddoux C., Procyk R., Grieninger G.;
"The beta chain of chicken fibrinogen contains an atypical thrombin
                                                                                                               NGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTPDRDNDRYP
                                                                                                                                                                                                                                                                                         MRLPGWLWLSSAVLAACRAVEEHNLTEGLEDASAQAACPARLEGSGRCEGSQCPFQLTLP
                                                                                                                                                                          SRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKVANLTVVVNSL
                                                                                                                                                                                                            DGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMETM
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                                                                                                                                                                                                                                                                                                                          SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
                                                                                     ;
0
                                                                     Length
                                                                                      Indels
                 f SIMILARITY.
f SIMILARITY.
-> G (IN REF. 2).
2B297F69CCB4A782 CRC64;
                                                                    Score 2340; DB 1;
Pred. No. 2.4e-163;
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Last annotation update)
PRECURSOR (FRAGMENT).
         PROTHROMBINASE
                                                                                     Mismatches
                  \mathbf{B}\mathbf{Y}
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100.0%;
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                                                                                     Conservative
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19
432
235
377
332
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BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 26,
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                                          432 AA;
                                                                             Similarity
20
206
364
332
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01-JUL-1993
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                                                                                    Matches 432;
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Q02020;
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                         DISULFID
                                                                    Query Match
Best Local
                 DISULFID
                                           SEQUENCE
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SIGNAL
         CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
SIMILARITY).
SIMILARITY).
SIMILARITY).
SIMILARITY).
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONTERTED INTO THE HARD CLOT BY FACTOR XITIA WHICH CAPALXZES THE EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 KEAVDSLKKSCQDCKLQADDHRDPGGNGGNGAETAEDSRVQELESQVNKLSSELKNAKDQ 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93;
                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00514; FIBRÎN_AG_C_DOMAIN; 1.
Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfatation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIRKINGER BETA CHAIN.
SULFATATION (BY SIMILARITY).
CLEAVAGE (BY THROMBIN, RELEAS,
FIBRINOPEPTIDE B).
INTERCHAIN (WITH ALPHA) (BY S
INTERCHAIN (WITH GAMMA) (BY S
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Pred. No. 8.2e-29;
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SIMILARITY.
SIMILARITY.
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BY
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HSSP; P02675: 1575
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PFAM; PF00147; fibrir
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437

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IFWGTWPGINQAQPGGYKSSFKQAKMMIRP 427

FTTPDRDNDRY - - - - PSGNCGLYYSSGWWFDSCLSANLNGKYY

ARLDGSTNFTREWKDYKAGFGNLER------EFWLGNDKIHLLTKSKEMILRIDL

EDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALR--FSRHYN-----HDLRF EDWNGDKVSALYGGFT IHNEGNKYQLSVSNYKGNAGNALMEGASQLYGENRTMT IHNGMY

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[16]
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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438 IVWMNWKG-----SWY--SMKKMSMKIKP 459
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13-AUG-1987 (Rel. 05, Last sequ
15-JUL-1999 (Rel. 38, Last anno
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                                                          STANDARD;
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P02679;
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MEDLINE-97169449; PubMed-9016719;
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MEDLINE-85261382; Pubmed-3160702;
                                                                                                                                                        MEDLINE=76225080; PubMed=936108;
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281 KIHLLTKSKEM--ILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNY-NGTAGDAL- 336
     198 LKANQQFLVYCEIDGSGNGWTVFQKRLDGSVDFKKNWIQYKEGFGHLSPTGTTEFWLGNE
                                                                                                                                                                                                         318 GFDFGDDPSDKF--FTSHNGMQFSTWDNDNDKF-EGNCAEQDGSGWMMNKCHAGHLNGYY
                                                                              DHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE----REFWLGND
                                                                                                                                                                                                                                                                                     -----RFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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MEDIJNE=88030379; PubMed=6092346;
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Crabtree G.R.;
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J. Blol. Chem. 259:12826-12830(1984).
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Wolfenstein-Todel C., Mosesson M.W.;
Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant (gamma') ";
Biochemistry 20:6146-6149(1981);
                                                                                                                                                                                                                                                                                                                                                                                     387 YH-----QKYKGVRNGIFWGTWPGINQAQPGCYKS---SFKQAKMMIRPKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human plasma fibrinogen heterogeneity: evidence for an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P04469; P04470;
21-JUL-1986 (Rel. 01, Created)
13-AUC-1987 (Rel. 05, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
FIBRINOGEN GAMMA-B CHAIN PRECURSOR (FIBRINOGEN GAMMA').
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Bantia S., Mane S.M., Bell W.R., Dang C.V.;
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X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 114-432.
                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 114-432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARÍANTS ASAHI; KYOTO-1; KYOTO-3 AND OSAKA-2.
MEDLINE-93043066; Pubmed-1421174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Invest. 83:1590-1597(1989).
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99175089; PubMed=10074346;
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                                                                                                                                                                                                      MEDLINE=98292395; PubMed=9628725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89214687; PubMed-2496144;
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                          MEDLINE=97472408; PubMed=9333233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 32.9 Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blood 75:1659-1663(1990)
                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT BERN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT ASAHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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us-09-442-143-4.rsp

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(ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BOND
ALTERNATIVE PRODUCTS: THIS CHAIN DIPERERS FROM THE GAMMA-A CHAI
AT RESIDARS 434-47 FOLLOWED BY 16 ADDITIONAL RESIDUES OF THE
CARBOXYL END. THESE DIFFERENCES ARE PRODUCED BY AN ALTERNATE
                                                                                                                                                                                                                                               SPLICING OF THE MRNA IN WHICH THE EIGHTH (LAST) INTRON IS NOT
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MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THOS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CATALYZES THE EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS OF DIFFERENT

MISCELLANEOUS: THE GAMMA-B CHAIN IS PRESENT IN ABOUT 10% OF THE FIBRINOGEN MOLECULES IN PLASMA BUT ABSENT FROM THOSE IN THE (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER)

PLATELETS.

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PFAM; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Blood coagulation; Glycoprotein; Calcium; Platelet; Plasma; Alternative splicing; Sulfatation; Signal. X02415; -; NOT_ANNOTATED_CDS. K02569; AAA52430.1; -. EMBL; M10014; AAB59530.1; -. INTERPRO; IPR002181; -. PIR; A03126; FGHUGB. HSSP; P02679; 1FZB. MIM; 134850; -. EMBL; X02415; EMBL;

AMINO END OF ALPHA-CHAIN OF ANOTHER N-LINKED (GLCNAC...).
INTERCHAIN (WITH C-35').
INTERCHAIN (WITH C-34').
INTERCHAIN (WITH C-110 IN BETA).
INTERCHAIN (WITH C-27') IN BETA).
INTERCHAIN (WITH C-22') IN BETA).
INTERCHAIN (WITH C-22') IN BETA). POLYMERIZATION SITE, BINDING TO CROSS-LINK TO 432-LYS AND 42 CROSS-LINK TO 432-LYS AND 42 SULFATATION (PROBABLE).

R -> Y (IN REF. 4).

Y -> R (IN REF. 4).

Y -> R (IN REF. 4). FIBRINGEN GAMMA-B CHAIN. FIBRIN MONOMER MM: 51496 453 78 34 35 45 45 101 105 208 26 444 435 448 453 AA; DISULFID DISULFID CONFLICT CARBOHYD DISULFID DISULFID DISULFID DISULFID CA_BIND SITE BINDING CONFLICT MOD_RES SIGNAL CHAIN

18; GSQCPFQL----TLPTLT1QLPRQLGSMEEVLKEVRTLKEAVDSLKKSCQDCKLQADDHR 105 Gaps 71; DB 1; Length 453; Indels Score 488.5; DB 1 Pred. No. 1.9e-28; 54; Mismatches 20.9%; 32.9%; Conservative Query Match Best Local Similarity 136; Matches 20 42 g δ

106 DPGGNGGNGAETAE-DSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIEN 164

ò g à

101 KP-----NMIDAATLKSRI--MLEEIMKYEASILTHDSSIRYLQ-----EIYNSNN---

165 YVDNKVANLTVVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTP

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"Complementary DNA sequence of lamprey fibrinogen beta chain.";
Biochemistry 25:6512-6516(1986).
-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET 280 (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XILIA WHICH CATALYZES THE EPSILCON-(CAMMA-GLUTAMYLLYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT LKANQQFLVYCEIDGSGNGWTVFQKRLDGSVDFKKNWIQYKEGFGHLSPTGTTEFWLGNE 257 KIHLLTKSKEM--ILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNY-NGTAGDAL- 336 ---RFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKY 386 DHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE----REFWLGND KIHLISTQSAIPYALRVELEDWNGRTSTADYAMFKVGPEADKYRLTYAYFAGGDAGDAFD Cottrell B.A., Doolittle R.F.; "Amino acid sequences of lamprey fibrinopeptides A and B and characterizations of the junctions split by lamprey and mammalian Petromyzon marinus (Sea lamprey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia; Petromyzontiformes; Petromyzontidae; Petromyzon. -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS 387 YH------QKYKGVRNGIFWGTWPGINQAQPGGYKS---SFKQAKMMIRPKN 01-FEB-1994 (Rel. 28, Last annotation update) FIBRINGEN BETA CHAIN (FRAGMENTS). 477 AA Biochim. Biophys. Acta 453:426-438(1976) Last sequence MEDLINE=87076582; PubMed=3790537; MEDLINE=77065679; PubMed=999898; Created) HSSP, P02675; IFZA. INTERPRO; IPR002181; -. PFAM; PF00147; fibrinogen_C; EMBL; M14773; AAA49261.1; -. SEQUENCE OF 37-477 FROM N.A. STANDARD; A25052; A25052. PIR; A03124; A03124 (Rel. (SEQUENCE OF 1-36. AGGREGATION. MONOMERS 01-OCT-1989 21-JUL-1986 FIBB_PETMA P02678; thrombins RESULT 5 FIBB_PETMA 145 225 281 258 337 a Οy g ò q δ g DDR N õ g

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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 YVANEFLKYRLHIGNYNGTAGDALRFSRHY------NHDLRFFTTPDRDNDRY----
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                                                                                                                                                                                                                                                                                       77;
                                                       SULFATATION.
N-LINKED (GLCNAC. ..).
INTERCHAIN (WITH THE ALPHA CHAIN)
                                                                                             (DI SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

INTERCHAIN (WITH THE GAMMA CHAIN)

(BY SIMILARITY).
                                                                                                                                                          (BY SIMILARITY).
INTERCHAIN (WITH THE GAMMA CHAIN)
                                                                                                                                                                                                                                                                  DB 1; Length 477;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                INTERCHAIN (WITH THE ALPHA
                                                                                                                                                                                                                                B8A95E7E32D09D18 CRC64;
PROSITE; PS00514; FIBRIN_AG_C_DOWAIN; 1.
Blood coagulation; Plasma; Sulfatation; Glycoprotein.
PEPTIDE 1 36 FIBRINOPEPTIDE B.
                                             FIBRINOGEN BETA CHAIN.
                                                                                                                                                                                                                                                               20.1%; Score 470.5; DB 1; 30.5%; Pred. No. 4.1e-27; ive 65; Mismatches 161;
                                                                                                                                                                                   SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
FIBRINOGEN GAMMA-B CHAIN PRECURSOR (GAMMA').
                                                                                           (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                     Conservative
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462 WY--SMRQMAMKLRPK 475
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477
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                         36
<37
13
27
84
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Best Local Simi
Matches 133;
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P12799;
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DISULFID
SEQUENCE
                                                        MOD_RES
CARBOHYD
                                   NON_CONS
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                                                                                                                                                                                                                                                            MONOMERS THAT
                                                                                                                                                                                                                                                                                                        -i- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-i- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGRED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA RESPONSTBLE FOR THE FORMATION OF THE SOFT CLOT: THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CATALYZES THE EPSILON - (GAMMA-GLOTAMYL) JYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STROWER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Blood coagulation; Glycoprotein; Calcium; Platelet; Plasma; Signal.
                                                                                                                                                   MEDLINE=77112616; PubMed-836881;
Timpl R., Fietzek P.P., Wachter E., van Delden V.;
"Disulfide-linked cyanogen bromide peptides of bovine fibrinogen. I
Isolation and sequence analysis of the chain constituents from the amino terminal region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 AACPARLEGSGRC-----EGSQCPFQL----TLPTLTIQLPRQLGSMEEVLKEVRTLKE
                                                                     ψ
                                                                                                                                                                                                                                        Biochim. Biophys. Acta 490:420-429(1977).
-!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOME! POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (PROBABLE).
BY SIMILARITY.
BY SIMILARITY.
                            MEDLINE-89386666; PubMed-2771651;
Brown W.M., Dziegielewska K.M., Foreman R.C., Saunders N.R.;
"Nucleotide and deduced amino acid sequence of a gamma subunit
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C-32').
BETA).
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Pred. No. 7.9e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                   Nucleic Acids Res. 17:6397-6397(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
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50244 MW;
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31.48;
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205
364
32
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PIR; S05313; S05313.
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Best Local Similarity
                 SEQUENCE FROM N.A.
                                                                                     fibrinogen.
                                                                                                                                      SEQUENCE OF 25-63.
                                                                                                                                                                                                                                                                                               AGGREGATION.
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56 CPKRISHSPEYP-----RDCYD--ILQSCSGQSPPSGQYYIQPDGGN-LIKVYCDMETD 106
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                                                                                                                                                                                                                                                                                                     418 FKQAKMMIR 426
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P02675;
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-!- SIMILARITY: RELATED TO THE C-TERMINAL PART OF THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
                                                                                                                                                                                                                                                                                                   412
                                                                                                                                                    230 NWIQYKEGFGHLSPTGTGNTEFWLGNEKIHLISTQSSIPYVLRIQLEDWNGRTSTADYAS 289
116 EIM-KYETLISTHESTIRFLQEVYNSNSQKIVNLRDKVVQLEANCQE-PCQDTVK---IH 170
                                                                                                                                 311
                                                                                                                                                                                                                                                                                                                                            397
                                                                   HLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTR
                                                                                                                            EWKDYKAGFGNL-----EREFWLGNDKIHLLTKSKEM--ILRIDLEDFNGLTLYALYDQ
                                                                                                                                                                                                               FYVANEFLKYRLHIGNY-NGTAGDAL------RFSRHYNHDLRFFTTPDRDNDRY
                                                                                                                                                                                                                                                                                                   360 PSGNCGLYYSSGWWFDSCLSANLNGKYYH-----QKYKGVRNGIFWGTWPGINQAQPG
                                                                                                                                                                                                                                                                                                                                          348 -DGNCAEQVGIGWWMNKCHAGHLNGVYYQGGTYSKTSTPNGYDNGIIWATW-----
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01-FEB-1991 (Rel. 17, Last séquence update)
15-JUL-1999 (Rel. 17, Last annotation update)
FIBRINGEN-LIKE PROTEIN A PRECURSOR (FREP-A).
Parastichopus parvimensis (Sea cucumber).
Eukaryota: Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Holothuroidea; Aspidochirotacea; Aspidochirotida; Stichopodidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
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79;
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                      413 GYKS---SFKQAKMMIRPKN 429
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224
282 AA;
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HSSP; P02671; 1FZD.
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P19477;
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Matches 106;
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SIGNAL
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FIBA_PARPA
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187 CPSQ-EHMQSQPVQHLIYKDCSDHYVLGRRS----SGAYRVTPDHRNSSFEVYCDMETM 240

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SEQUENCE FROM N.A.
MEDLINE-83283433; PubMed-6688356;
Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;
Characterization of complementary deoxyribonucleic acid and genomic deoxyribonucleic acid for the beta chain of human fibrinogen.";
Blochemistry 22:3244-3250(1983).
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"Human fibrinogen: sequence, sulfur bridges, glycosylation and some
structural variants.";
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Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
Pergamon Press, Oxford (1980).
                   NGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTPDRDNDRYP
                                                                                                                                                        241 GGGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEMILRIDLEDF
                                                                                                                                     SGNCGLYYSSG---WWFDSCLSANLNGKYYHQKYKGVRNGIFWGTWPGINQAQPGGYKSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-91344740; PubMed=2102623;
Chung D.W., Harris J.E., Davie E.W.;
"Nucleotide sequences of the three genes coding for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) FIBRINGEN BETA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                          491 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exp. Med. Biol. 281:39-48(1990).
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                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created) 01-JUL-1993 (Rel. 26, Last seq) 01-OCT-2000 (Rel. 40, Last ann
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Homo sapiens (Human).
Motazoa; Chordata;
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SEQUENCE OF 1-38 FROM N.A.
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Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.; "Conformational changes in fragments D and double D from human fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide."; Biochemistry 38:2941-2946(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.; "Crystal structure of fragment double-D from human fibrin with two different bound ligands."; Biochemistry 37:8637-8642(1998).
                                   'Characterization of the 5'-flanking region for the human fibrinogen
                                                                                                                                                                                                                                                                                                                     Cottrell B.A., S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
Asakura S., Shirakawa S.;
                                                                                                                                                                                                                                              В.;
                                                                                                                                                                                                                                                                                                                                                                             Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spraggon G., Everse S.J., Doolittle R.F.; "Crystal structures of fragment D from human fibrinogen and its crosslinked counterpart from fibrin."; Nature 389:455-462(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schmelzer C.H., Ebert R.F., Bell W.R.;
"A polymorphism at B beta 448 of fibrinogen identified during structural studies of fibrinogen Baltimore II.";
                                                                                              Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton "Studies on fibrinopeptides from primates."; Acta Chem. Scand. 19:1788-1789(1965).
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Eur. J. Blochem. 77:595-610(1977).
             Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z.,
                                                                                                                                                                                                                                                                                                                    Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cassman K.G., Goldbaum D.M., Doolittle L.R., Friezner He structures of fibrinogen and fibrin, ", (In) Magnusson S., Ottesen M., Foltmann B., Dano K.,
                                                                                                                                                                                                                                                                                                                                                                                                                 REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
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                                                                                                                                            REVIEW, AND DISULFIDE BONDS.
MEDLINE-83254370; PubMed=6575689;
Henschen A., Lottspeich F., Kehl M., Southan C.;
"Covalent structure of fibrinogen.";
Ann. N.Y. Acad. Sci. 408:28-43(1983).
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                                                           Nucleic Acids Res. 15:1615-1625(1987)
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MEDLINE=89058942; PubMed=3194892;
MEDLINE=87146483; PubMed=3029722;
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=84305751; PubMed=6383194;
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MEDLINE=91208409; PubMed=2018836;
                                                                                                                                                                                                                                                                                                                                                                                           ergamon Press, New York (1978).
                                                                                                                                                                                                                                 MEDLINE=77245999; PubMed=891553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thromb. Res. 52:173-177(1988)
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                                                                                  SEQUENCE OF 31-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENDS OF THE ALPHA CHAINS.

-1- DISEASE: DEFECTS IN FGB ARE A CAUGE OF THROMBOPHILIA.

-1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CATALYZES THE EPSILON (GAMMA-GLOTPANYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                               VARIANT NAPLES.
MEDIINE=92340664; PubMed=1634610;
Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
"Molecular basis of fibringen Naples associated with defective thrombin binding and thrombophilia. Homozygous substitution of B beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE. DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
                                                                                                                                                                                                                                                                                                                                                                       Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I., Rerst A.F., Joh., Lord S.T.; "Abnormal fibrinogens Ijmuiden (B beta Arg14-->Cys) and Nijmegen (B beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
replacement of B beta glycine-15 by cysteine.";
Blood 77:1958-1963(1991).
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X05018; CAA28674.1; -.
                                                                                                                                                                                                                                                       Clin. Invest. 90:238-244(1992).
                                                                                                                                                                                                                                                                                                            VARIANTS IJMUIDEN AND NIJMEGEN.
MEDLINE-92228809; PubMed-1565641;
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AAA52445.1;
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                                                                                                                                                                                                                                  68 Ala-->Thr.
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                                                                                                                                                                            136 ELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKV----ANLTVVVNSLDGKCSKCPSQ 190
                                                                                                                                                                                                   175 ELE--KHQL-------YIDETVNSNIPTNLRVLRSILENLRSKIOKL 212
                                                                                                                                                                                                                                      213 ESDVSAQMEYCRTPCTVSCNIPVVSGRECEEIIRKGGETSEMYLIQPDSSVKPYRVYCDM 272
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                                                                                                                                                                                                                                                                                                                     TKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHY--- 342
                                                                                                                                                                                                                                                                                                                                   92 KSCQDCKLQADDHRDPGGNGGNGAETAEDS-------RVQELESQVNKLSS 135
                                                                                                                                                                                                                          EHMQSQPVQH------LIYEDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDM 237
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                                                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Martinelli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
Hurrell J.G.R., Leach S.J., Scheraga H.A.;
"Amino acid sequences of portions of the alpha and beta chains of
bovine fibrinogen.";
                                                                                                                                                                                                                                                                                                                                                                   343 -----NHDLRFFTTPDRDNDRY----PSGNCGLYYSSGWWFDSCLSANLNGKYY----
                                 Score 463; DB 1; Length 491;
Pred. No. 1.5e-26;
60; Mismatches 151; Indels 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                              453 TWDMAKHGTDDGVVWMNWKG----SWY--SMRKMSWKIRP 486
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SEQUENCE OF 5-21.
Sjoquist J., Blomback B., Wallen P.;
"Amino acid sequence of bovine fibrinopeptides.";
Ark. Kemi 16:425-436(1960).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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 INTERPRO; IPR002181; -. PFAM; PF00147; fibrinogen_C; 1.
                                   tch 19.8%; sal Similarity 28.4%; 131; Conservative 6
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IPR002181;
                                               Local Similarity
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SEQUENCE OF 22-53.
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                                    Query Match
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SEQUENCE OF 44-468 FROM N.A. MEDLINE-81199473; PubMed=6262803; Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.; Chung D.W., Rixon A.W. Gillivray R.T.A., Davie E.W.; "Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen."; Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).

-:- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                           -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- MISCELLAMBOUS: CONVERSION OF FIRENTWOGEN TO FIBERIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBELNODEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSTBLE FOR THE FORMATION OF THE SOFT CLOT: THE SOFT CLOT
CONVERTED INTO THE HAND CLOT BY FACTOR XIIIA WHICH CATALYZES THE
EPSILON-(GAMMA-GLOTAMYL)IXSINE CROSS-LINKING BETWEEN GAMMA CHAINS
(STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
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2DED42F443AA4B37 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBRINOPEPTIDE B.
FIBRINOGEN BETA CHAIN.
PYRROLIDONE CARBOXYLIC ACID.
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CLEAVAGE (BY THROMBIN; RELIFIBRINOPEPTIDE B).
INTERCHAIN (WITH ALPHA).
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THERPRO. 1FR002181; -.
PFAM: PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
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Best Local Similarity
Matches 123; Conserv
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Pergamon Press, Oxford (1980).
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"Human fibrinogen: sequence, sulfur bridges, glycosylation and some
structural variants.";
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Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
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                                        NEFLKYRLHIGNYNGTAGDAL-----PSG
                                                                                363 NCGLYYSSGWWFDSCLSANLNGKYY-----HQKYKGVRNGIFWGTWPGINQAQPGGYK
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ALPHA-E FORM).
MEDLINE=93090725; PubMed=1457396;
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Roy S.N., Redman C.M., Grieninger G.,
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MEDLINE=83247396; PubMed=6575389;
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(In) Ebert R.F. (eds.);
Index of variant human fibrinogens, pp.13-24, CRC Press,
                                                                                                                                                                                                                              (Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
LPHA/ALPHA-E CHAIN PRECURSOR.
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                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                    FIBRINOGEN ALPHA/ALPHA-E
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-SMKKMSMKIRP 463
                                                                                                                         SSFKQAKMMIRP 427
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01-0CT-2000
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Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
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Exact location of cross-linking acceptor sites.";
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MEDLINE=84069777; PubMed=6669067;
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Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards
"The structure of residues 7-16 of the A alpha-chain of human fibrinogen bound to bovine thrombin at 2.3-A resolution.";
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MEDLINE-87057190; PubMed=2877981;
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Acta Chem. Scand. 19:1788-1789(1965).
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"Cross-linking site in fibrinogen for
J. Biol. Chem. 261:15591-15595(1986).
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MEDLINE=84104274; PubMed=6318767;
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thrombophilia.";
J. Clin. Invest. 91:1637-1643(1993).
-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
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Spraggon G., Applegate D., Everse S.J., Zhang J.Z., Veerapandian
Redman C., Doolittle R.F., Grieninger G.;
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                  Spraggon G., Everse S.J., Doolittle R.F.; "Crystal structures of fragment D from human fibrinogen and its crosslinked counterpart from fibrin."; Nature 389:455-462(1997).
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                                                                                                                                                                                                                                                                                                                                  "Crystal structure of a recombinant alphaEC domain from human fibrinogen-420.";
                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
MEDLINE=98292395; Pubmed=9628725;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99175089; PubMed=10074346;
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MEDLINE=97472408; Pubmed=9333233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blood 78:149-153(1991).
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SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE. DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH

AGGREGATION.

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                                                                                                 623 HAKSRPV----RDCDD--VLQTHPSGTQSGIFNIKLPGSSKIFSVYCDQETSLGGWLLI 675
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                                                                                                                                                                                                                      RYPSGNCGLYYSSGWWFDSCLSANLNGKYY -----HQKYKGVRNGIFWGTWPGINQ 408
                                                                                                                                                                                                                                                                                           Crabtree G.R., Comeau C.M., Fowlkes D.M., Fornace A.J. Jr., Malley J.D., Kant J.A.;
"Evolution and structure of the fibrinogen genes. Random insertion of
                                                                                                                                   QARLDGSTNFTREWKDYKAGFGNL----EREFWLGNDKIHLLTKSKEMILRIDLEDFNGL 303
                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDILINE=87134033; Pubbed=3817019;
Sobczak J., Lotti A.-M., Taroux P., Duguet M.;
"Molecular cloning of mRNA sequences transiently induced during rat liver regeneration.";
                                                                192 HMQSQPVQHLIYKDCSDHYVL----GRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVL
                                                                                                                                                                                                   304 TLYALYDQFYVANEFLKYRLHIGNYNGTAGDAL-----RFSRHYNHDLRFFTTPDRDND
                               42;
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 Length 866;
                                 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Fu Y., Cao Y., Hertzberg K., Grieninger G.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
Score 454; DB 1;
Pred. No. 1.4e-25;
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Last annotation update)
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"Studies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
                                 41; Mismatches
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SEQUENCE FROM N.A. (ALPHA FORM)
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01-OCT-1996 (Rel. 34, Last seq
19.48;
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J. Mol. Biol. 185:1-19(1985).
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                                 102; Conservative
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               Similarity
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                           PTM: THE ALPHA CHAIN IS NOT GLYCOSYLATED.

MISCELLAMENDUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMEIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERFED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CAPALYZES THE EPSILON-(GAMAA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHVPEFSSSSKTSTVRKQVTKSYKMADEAASEAHQEGDTRTTRRGRARTMRDCDD--VLQ 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH C-48') (BY SIMILARITY).
INTERCHAIN (WITH BETA) (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
INTERCHAIN (WITH BETA) (BY SIMILARITY).
INTERCHAIN (WITH C-165 IN GAMMA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- ESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 LTHSFSGRLDELSRMHPELGSFYDSRFGSLTSNFKEFGSKTS-----DSD1FTD1ENPS 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYV-----DNKVANLTVVVNSLDGKCSKCPSQEHMQ-----SQPVQHLIYKDCSDHYVLG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 TIGSDDTGTWGAGSSRPSSGGNLKPSNPDWGEFSEFGGSSSP-ATRKEYHTGKLVTSKG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMEEVLKEVRTLKEAVDSLKKSCQ----DCKLQADDHR-----DPGGNGGNGAET- 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
INTERCHAIN (WITH BETA) (BY SIMILARITY).
BY SIMILARITY.
DCDD -> GIHA (IN ISOFORM ALPHA).
MISSING (IN ISOFORM ALPHA).
EAGGD -> DEGAG (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 TEGLEDASAQACPAR-LEGSGRCE-----GSQCPFQLTLPTLT1QLPRQLG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blood coagulation; Plasma; Platelet; Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLEAVAGE (BY THROMBIN; RELEASE FIBRINOPEPTIDE A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>5</u>
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-E AND ALPHA; ARE PRODUCED BY ALTERNATIVE SPLICING. THE ALPHA FORM IS THE PREDOMINANT FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 452; DB 1; Length 782;
Pred. No. 1.7e-25;
68; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LREEIYÓ (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> K (IN REF. 4).
744834DAE76D34C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBRINGEN ALPHA-E CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBRINOPEPTIDE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> E (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASRGDLP ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                               EMBL; X86561; CAA60264.1; -. EMBL; X86561; CAA60263.1; -. EMBL; M35601; AAA41158.1; -.
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28.9%;
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782
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181
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56
65
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Best Local Simi
Matches 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOI. Cell. Endocrinol. 72:213-220(1990).
-!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-1- MISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGREED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSTBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CAPALYZES THE
EPSILON-(GAMMA-GLOTPAMYL)JYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
(STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                 NL----EREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHI 325
                                                                                                      326 GNYNGTAGDAL-----RFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLS 379
                                                                                                                                                                                        Bhattacharya A., Shepard A.R., Moser D.R., Holland L.J., "Isolation and characterization of cDNA clones for the gamma subunit of Xenopus fibrinogen, the product of a coordinately regulated gene
                                                                                                                                                                                                                                                                         380 ANLNGKYY------HQKYKGVRNGIFWGTWPGINQAQPGGYKSSFKQAKMMIRP 427
214 RRSSGA----YRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFG
                                      554 THPSGAQNGIFSIKLPGSSKIFSVYCDQETSLGGWLLIQQRMDGSLNFNRTWQDYKRGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90241882; PubMed-2334684;
Pastori R.L., Moskaitis J.E., Smith L.H. Jr., Schoenberg D.R.;
"Estrogen regulation of Xenopus laevis gamma-fibrinogen gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91146806; PubMed=2289632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBRINOGEN GAMMA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression.";
Biochemistry 29:2599-2605(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (Rel. 15, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-58 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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INTERPRO; IPR002181; -.
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           15;
                                           FIBRINOGEN GAMMA CHAIN.
INTERCHAIN (WITH C-33') (BY SIMILARITY).
INTERCHAIN (WITH C-32') (BY SIMILARITY).
INTERCHAIN (WITH BETA) (BY SIMILARITY).
INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
                                                                                                                                                                                                                                                        307
                                                                                                                                                                                                                                                                                                                                                            LYDQFYVANEFLKYRLHIGNY-NGTAGDAL------RFSRHYNHDLRFFTTPDRD 355
                                                                                                                                                                                                         74 EEVLKEVRTLKEAVDSLKKSCQDCKLQADDHRDPGGNGGNGAETAEDSRVQELESQVNKL 133
                                                                                                                                                                                                                           ENVDTDLQYLENLLTQISNSTSGTTIIVEHLIDSGKKPATSPQTAIDPMTQKSKTCWMKL 117
                                                                                                                                                                                                                                              134 SSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKVANLTVVVNSLDGKCSKCPSQEHM 193
                                                                                                                                                                                                                                                                                                                                                                                                NDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYH------QKYKGVRNGIFWGTWPGIN 407
                                                                                                                                                                                                                                                                                                                                                                                                                 342 NDKF-DGNCAEQDGSGWWMNRCHAAHLNGKYYQGGTYSEADSGPSGYDNGIIWATW---- 396
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
PFAM; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Blood coagulation; Glycoprotein; Calcium; Plasma; Platelet; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.; "Cloning of the complete coding sequence of rat fibrinogen B beta chain cDNA: interspecies conservation of fibrin beta 15-42 primary
                                                                                                                                                                                                                                                                                              STNFTREWKDYKAGFG----NLEREFWLGNDKIHLLTKSKEM--ILRIDLEDFNGLTLYA
                                                                                                                                                                                                                                                                                                                                  QSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDG
                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                       51;
                                                                                                                                                                     DB 1; Length 438;
                                                                                                                                                                                       60; Mismatches 149; Indels
                                                                                                                                N-LINKED (GLCNAC. . .) (P
69B1F01BB6716F60 CRC64;
                                                                                                                                                                              Pred. No. 1.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
FIBRINGEN BETA CHAIN PRECURSOR.
                                                                                                              SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lood Coagul. Fibrinolysis 5:487-496(1994).
                                                                                                                                                                     Score 448.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95143386; PubMed-7841303;
                                                                                                                                                                                                                                                                                                                                                                                                                                     QAQPGGYKSSFKQAKMMIRPKN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 -- RRRWY -- SMKSVTMKIMPLN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
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M
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31.9%;
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50064
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SEQUENCE OF 1-26 FROM N.A.
                                                                                                                                                                                        Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                     25
438
32
33
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47
162
205
362
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162
176
349
76
                                                                                                                                                                              Similarity
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01-0CT-1996
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P14480;
                                                                                                                                                                    Query Match
                                                                                                    DISULFID
                                                                                                                                CARBOHYD
                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

-I- MISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPETIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=WISTAR; TISSUE-LIVER;
MEDLINE=87134033; PubMed=3817019;
Sobczak J., Lotti A.-M., Taroux P., Duguet M.;
"Molecular cloning of mRNA sequences transiently induced during rat liver regeneration.";
Exp. Cell Res. 169:47-56(1987).
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 183-479 FROM N.A.
MEDLINE-89378771; PubMed-2673932;
Eastman E.M., Gilula N.B.;
"Cloning and characterization of a cDNA for the B beta chain of
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                        Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.; "Potential basis for regulation of the coordinately expressed fibrinogen genes: homology in the 5' flanking regions."; broc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
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N-LINKED (GLCNAC. ..) (POTILIS.
LSI -> ILS (IN REF. 3).
L -> Q (IN REF. 5).
S -> A (IN REF. 5).
S -> A (IN REF. 5).
R -> K (IN REF. 5).
W -> F (IN REF. 5).
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INTERCHAIN (WITH THE GAMMA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibrinogen: evolutionary conservation of translated and 3'-untranslated sequences.";
Gene 79:151-158(1989).
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Blood coagulation; Plasma; Glycoprotein; Signal.
                                                                                                                                               [3]
SEQUENCE OF 19-32.
Blomback B., Blomback M., Grondahl N.J.;
Bludies on fibrinopeptides from mammals.";
Studies or ibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
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MEDLINE-84194000; PubMed-6232608;
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EMBL; M27220; AAA41160.1; -.
EMBL; K01336; AAA98625.1; -.
EMBL; M35602; AAA41159.1; -.
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PIR; PE0010; PE0010.
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479 AA;
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-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                 246
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE-84194000; PubMed=6232608;
FOWIKES D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
FOWIKES D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
FOCHOTIAL basis for regulation of the coordinately expressed fibrinogen genes: homology in the 5' flanking regions.";
Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
          Length 479;
                                                                  Indels
   ; Score 444; DB 1; L.; Pred. No. 3.5e-25; 48; Mismatches 118;
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"Nucleotide sequence of the gamma chain gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
FIBRINGGEN GAMMA-A/-B CHAIN PRECURSOR.
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Nucleic Acids Res. 15:2774-2776(1987).
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MEDLINE=83129318; PubMed=6897622;
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                                 Local Similarity 32.6
nes 116; Conservative
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MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CAPALYZES THE EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (TRENGER) OF DIFFERENT
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INTERCHAIN (WITH THE ALPHA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH THE BETA CHAIN)
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INTERCHAIN (WITH THE GAMMA CHAIN)
(BY SIMILARITY).
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(BY SIMILARITY).
INTERCHAIN (WITH THE GAMMA CHAIN)
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BY SIMILARITY
BY SIMILARITY.
SYE -> GDM (IN GAMMA-A CHAIN).
MISSING (IN GAMMA-A CHAIN).
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PROSTIE; PS0514; FIBRIN_AG_C_DOMAIN; 1.
Blood coagulation; Glycoprotein; Calcium; Platelet; Plasma; Alternative splicing; Signal.
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Mismatches 130
                                                                                                                                                       the European Bioinformatics Institute. There use by non-profit institutions as long a modified and this statement is not removed.
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       EMBL; J00733; -; NOT_ANNOTATED_CDS.
EMBL; J00734; -; NOT_ANNOTATED_CDS.
EMBL; J00735; -; NOT_ANNOTATED_CDS.
EMBL; X05860; CAA22289.1; -
EMBL; X05861; CAA2289.1; JOINED.
EMBL; K01337; AAA98626.1; -.
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SIGNAL 1
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PIR; A03128; FGRTGB.
HSSP; P02679; 1FID.
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445 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takagi T., Finlayson J.S., Iwanaga S.;
"Amino acid sequence of chicken fibrinopeptide A.";
Biochim. Biophys. Acta 534:161-144(1978).
-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: XIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
   ----RESRHYNHDLRFFTTPDRDNDRYP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPERTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                    292 RVGPESDKYRLTYAYFIGGDAGDAFDGYDFGDDPSDKF--FTSHNGMHFSTWDNDNKF- 348
                                                                                         361 SGNCGLYYSSGWWFDSCLSANLNGKYYH-----QKYKGVRNGIFWGTWPGINQAQPGG 413
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGREGATION.
SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
ALTERNATIVE PRODUCTS: 2 ISOFORMS, ALPHA-E AND ALPHA; ARE
PRODUCED BY ALTERNATIVE SPLICING. THE ALPHA FORM IS THE
PREDOMINANT FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weissbach L., Grieninger G.; "Bipartite mRNA for chicken alpha-fibrinogen potentially encodes an amino acid sequence homologous to beta- and gamma-fibrinogens."; Proc. Natl. Acad. Sci. U.S.A. 87:5198-5202(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Greininger G.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                    741 AA.
 313 YVANEFLKYRLHIGNY-NGTAGDAL----
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 5-741 FROM N.A. MEDLINE=90311369; PubMed=2367530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB60686.1; JOINED.
AAB60686.1; JOINED.
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AAB60685.1; JOINED.
AAB60685.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 19-33.
MEDLINE-78187470; PubMed-656462;
                                                                                                                                            414 YKS---SFKQAKMMIRPKN 429
                                                                                                                                                                           399 -KTRWYSMKETTMKIIPFN 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U20803; AAB60686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB60685.1;
AAB60685.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-4 FROM N.A.
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    020803;
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                                                                                                                                                                                                                                                                   FIBA_CHICK
                                                                                                                                                                                                                                RESULT 15
FIBA_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus
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EMBL;
EMBL;
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Search completed: February 27, 2001, 12:52:04 Job time: 235 sec

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11;
                                                                                                  FIBRINOPEPTIDE A.
FIBRINOGEN ALPHA-E CHAIN.
PYRROLIDONE CARBOXYLIC ACID.
INTERCHAIN (WITH C-42') (BY SIMILARITY).
INTERCHAIN (WITH THE BETA CHAIN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 KDCSD---HYVLGRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRE 260
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   261 WKDYKAGFGNL----EREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVAN
                                                                                                                                                                                                                                                                                                                                                                                                                                              EFLKYRLHIGNYNGTAGDAL ----RFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GWWFDSCLSANLNGKY - - - - - YHQKYK - - - GVRNGIFWGTWPGINQAQPGGYKSSFKQAK
                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                        INTERCHAIN (WITH THE GAMMA CHAIN)
(BY SIMILARITY).
                                                                                                                                                                                   (BI SIMILMAKIII).
THERCHAIN (WITH THE BETA CHAIN)
(BY SIMILMARITY).
INTERCHAIN (WITH THE GAMMA CHAIN)
                                                                                                                                                                                                                                                                                                                                              Length 741;
                                                                                                                                                                                                                        (BY SIMILARİTY).
INTERCHAIN (WITH THE BETA CHAIN)
(BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                   CLEAVAGE (BY THROMBIN; RELEASE
FIBRINOPEPTIDE A).
DCDD -> GTQK (IN ISOFORM ALPHA).
MISSING (IN ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                             18.4%; Score 431.5; DB 1; Length ilarity 39.2%; Pred. No. 5.1e-24; Conservative 39; Mismatches 77; Indels
                                             INTERPRO; IPR002181; -.
PFAM; PF00147; fibrinogen_C: 1.
PROSITE; PS00514; FIBRIN_AG_C_DOWAIN; 1.
Blood coagulation; Plasma; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                               A09F5F4F186DE3A6 CRC64;
    AAB60685.1; JOINED.
                                                                                                                                                                                                                                                                                                     741 M
82438 MW;
EMBL; U20802; AAB60685.1; Jr
EMBL; M34096; AAA99306.1; -
EMBL; M34096; AAAA9307.1; -
HSSP; PO2671; IFZD.
INTERPRO; IPR002181; -
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Best Local Si
Matches 96;
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VARSPLIC
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GenCore
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 protein search, using sw model protein ĕ

February 27, 2001, 12:50:10 ; Search time 31.84 Seconds (without alignments) 921.265 Million cell updates/sec Run on:

US-09-442-143-4 Title: Perfect sc Sequence:

2340 1 MRLPGWLWLSSAVLAACRAV......GYKSSFKQAKMMIRPKNFKP 432 score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 seqs, 67900655 residues Searched: 195891 hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		cytotoxic T-lympho	fibrinogen-like pr		u					fibrinogen gamma-B		ficolin-A precurso	fibrinogen beta ch					യ	ficolin-beta - piq	transforming growt	a)	fibrinogen gamma c		fibrinogen gamma-A			tenascin-x precurs	tenascin homolog -	tenascin-X - pig (tenascin-X - bovin
SUMMARIES		A27447	I56934	137391	JN0596	A38463	FGHUG	FGHUGB	A25052	S05313	A35084	JC5980	FGHUB	FGBOB	JH0675	D44234	A32670	A45445	B47172	A47172	S61517	FGLMGS	A05299	FGRTGA	FGRTGB	A32230	A40701	S28170	94	T42629
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Result No.	1	Т	7	m	4	ស	9	7	œ	σ			12		14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

tenascin precursor	tenascin precursor	tenascin-C numan tenascin-X - mouse	probable tenascin	tenascin Y precurs	fibrinogen alpha-I	· scabrous locus (sc	scabrous protein p	hypothetical prote	hypothetical prote	hypothetical prote	microfibril-associ	hypothetical prote	hypothetical prote	hypothetical prote
J01322	S19694	148839	T09070	T42635	A41932	A39832	858888	T15876	T21773	T21772	PC2036	T29850	T26827	T32255
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17.5	17.5	17.2	17.2	16.9	16.0	15.9	15.9	9.6	9.8	9.8	8.1	7.3	7.2	7.1
409	408.5	402.5	402.5	395.5	374	372.5	372.5	224.5	200.5	200.5	189.5	170	169	165.5
30	32	3 6	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

Gaps ö Length 432; Indels Query Match 100.0%; Score 2340; DB 2; Best Local Similarity 100.0%; Pred. No. 1.7e-159; Matches 432; Conservative 0; Mismatches 0;

6

Qy	1 MRLPGWLWLSSAVLAACRAVEEHNLTEGLEDASAQAACPARLEGSGRCEGSQCPFQLTLP 60
qa	1 MRLPGWLWLSSAVLAACRAVEEHNLTEGLEDASAQAACPARLEGSGRCEGSQCPFQLTLP 60

g ò

180 SRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKVANLTVVVNSL 121 g ò

DGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMETM 240 181 181 q δý

300 300 GGGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEMILRIDLEDF 241 GGGWTVLQARLDGSTNFTREWKDYRAGFGNLEREFWLGNDKIHLLTKSKEMILRIDLEDF 241 qq ò

NGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTPDRDNDRYP 360 301 g δ

420 SGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKGVRNGIFWGTWPGINQAQPGGYKSSFKO 361 361 g ò

421 AKMMIRPKNFKP 432

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C; Accession: JN0596
R; Yamamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem: Blophys. Res. Commun. 193, 681-687, 1993
A; Title: Molecular cloning and initial characterization of a novel fibrinogen-related A; Reference number: JN0596; MUID: 93290661
A; Accession: JN0596
A; Molecule type: mRNA
A; Residues: 1-312 < YAM>A; Residues: 1-312 < YAM>A; Residues: 1-312 < YAM>A; Cross-references: GB:D14446; NID: 9393314; PIDN: BAA03336.1; PID: 9393315
A; Experimental source: liver
C; Superfamily: fibrinogen beta/gamma homology
F; 1-17/Domain: signal sequence #status predicted <SIG>F; 1-17/Domain: signal sequence man homology
F; 1-18-312/Product: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
                                                      A;Cross-references: EMBL:236531; NID:9535184; PIDN:CAA85298.1; PID:9535185
A;Note: submitted to the EMBL Data Library, August 1994
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F;210-435/Domain: fibrinogen beta/gamma homology <FBG.
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                                                                                                                                                                                                                                                                                                                                                                    121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVCHGRLEKLNLVNMNNIENYVDSKVANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRLPGWLWLSSAVLAACR-AVEEHNLTEGLEDASAQAACPARLEGSGRC-EGSQCPFQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 LPTLTIQLPRQLGSMEEVLKEVRTLKEAVDSLKKSCQDCKLQADDHRDPGGNG----GNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE-TAEDSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKVANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIDLEDFNGLFLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKGVRNGIFWGTWPGINQAQPGG
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                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                       1853.5; DB 2;
No. 8.5e-125;
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                                                                                                                                                                                                                                                                                      49:
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; Pred. No. 8.5e
42; Mismatches
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341; Conservative 4
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R; Parr, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, J. Virol. 69, 5033-5038, 1995
A; Title: Association of mouse fibrinogen-like protein with murine hepatitis v A; Reference number: 156934; MUID:95333285
A; Accession: 156934
A; Molecule type: mRNA
A; Residues: 1-432 CRES>
A; Cross-references: GB:S78773; NID:g1042169; PIDN:AAB34823.1; PID:g1042170
C; Genetics:
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                                                                                                                                                                   C;Species: Mus sp. (mouse)
C;Date: 26-Jul_1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
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C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma
F;203-428/Domain: fibrinogen beta/gamma homology <FBG>
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Pred. No. 3.2e-159;
0; Mismatches 1;
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99.8%;
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OV 349 PTTPDBPNDRVPGGNCTIVVSGGWBFDGCTSANT.NGRVV	378 FSTYDRDNDGWLTT	Qy 398 IFWGTWPGINQAQPGGYKSSFKQAKMMIRP 427 1 1 1 1 1 1	RESULT 6 FGHUG	fibrinogen gamma-A chain precursor - human N;Alternate names: coagulation factor I C;Species: Homo sapiens (man) C;Date: 24-Apr.1984 #sequence_revision 25-Feb-1985	C; Accession: A90470; B90494; C94433; B93956; B92448; I3735 R; Chung, D.W.; Chan, W.Y.; Davie, B.W. Biochemistry 22, 3250-3256, 1983 A; Title: Characterization of a complementary deoxyribonucl	A; Reference number: A90470; MUID:83283434 A; Accession: A90470 A; Molecule type: mRNA A; Residues: 1-437 < CHO>	A; Residues: 1-113,'I'.115-437 <rix> A; Cross-references: GB: XO2415; GB: M10014; NID: 9182438; PII R; Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Peters in Protides of the Biological Fluids, Proc. 28th Colloq., A; Title: Human fibrinogen: sequence, sulfur bridges, glycc A; Title: Human fibrinogen: sequence, sulfur bridges, glycc</rix>			A. Residues: 276-437 <kan> R. Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; R. Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; J. Biol. Chem. 259, 12826-12830, 1984 A. Title: Structure of the human gamma-fibrinogen ge</kan>	A; Accession: B92448 A; Accession: B92448 A; Molecule type: DNA A; Residues: 286-437 < FOR>	R; Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, Nucleic Acids Res. 11, 742-7434, 1983 A; Title: Isolation and characterisation of cDNA clones for A; Reference number: 137393; MUID:84069777	A:Accession: 137393 A:Status: preliminary; translated from GB/EMBL/DDBJ A:Nolecule type: mRNA A:Residues: 209-270 <res></res>	A;Cross-references: EMBL:X00086; NID:931445; PIDN:CAA24944 R;Bertagnolli, M.E. Beckerle, M.C. J. Cell Biol. 121, 1329-1342, 1993 A;Title: Evidence for the selective association of a subpc	A; Reference number: A40698; MUID:93286185 A; Accession: A40698 A; Molecule type: protein A; Residues: 27-33,'XX',36-41 <ber></ber>	A; Experimental source: thrombin-activated platelets A; Note: sequence extracted from NCBI backbone (NCBI R; Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter,
115 AETAEDSRVOELESOVNKLSSELKNAKDOIOGLOGRLEFTLHLVNMNNIENVVDNKVANLF 174	:: :::: :: :: :: :: :: ::	175 VVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVY 234	235 CDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEM 291			GINQAQPGGYKSSFKQAKMMIRPKNFKP 432 	C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999 C;Accession: A38463 B34643 C;Accession: A38463 C;Accession: A38463 C;Accession: A;Welssbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G. Biochemistry 30, 3299-3294, 1991 A;Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage A;Reference number: A38463; MUID:91182745	A,Accession: A38463 A,Status: preliminary A;Molecule type: mRNA A;Residues: 1-463 <wei> A;Cross-references: CB:MG8514: NID.4211779: DIDN.abaA8770 1: DID.4211780</wei>	Juga interestry of the parameter of the	Query Match 21.1%; Score 493.5; DB 2; Length 463; Best Local Similarity 30.4%; Pred. No. 8.9e-28; Matches 137; Conservative 58; Mismatches 162; Indels 93; Gaps	30 EDASAQAACPARLEGSGRCEGSQCPFQLTLPTLTIQLPRQLGSMEEVLKEVRTL 83 :	84 KEAVDSLKKSCQDCKLQADDHRDPGGNGAETAEDSRVQELESQVNKLSSELKNAKDQ 143	144IQGLQGRLETLHLVNMNIENYDDNKVANLTVVVNSLDGKCSKCPSQEHMQSQ 196 : : :	197PVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMETWGGGWTVLQ 248 200 PCVASCNIPVVSGRECEDIYRKGGETSEMYIIQPDPFTTPYRVYCDMETDNGGWTLIQ 257	249 ARLDGSTNFTREWKDYKAGFGNLERFWLGNDKIHLLTRSKEMILRIDL 297 1 1 1 1 1 1 1 1 1	298 EDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRF 348

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7393; A40698; H54223; A03125;
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GTYSWDMAKHGTDDG 437
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A;Accession: A90494
A;Molecule type: DNA
A;Residues: 1-113,'I',115-453 <RIX>
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R; Kloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.
Biochemistry 23, 1767-174, 1984
A; Tile: Platelet receptor recognition site on human fibrinogen. Synthesis and structure
A; Reference number: A90483; MUID:84203545
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R; Plow, E.F.; Srouji, A.H.; Meyer, D.; Marguerie, G.; Ginsberg, M.H.
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A; Reference number: A92477; MUID:84185664
A; Contents: annotation; platelet aggregation region
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A; Title: Localization of a fibrinogen calcium binding site between gamma-subunit positic
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                                                                             A) Title: Fibringen and fibrin.
A) Reference number: 89004; MUID: 84305751
A) Contents: annotation; review, EM structure, polymerization, ligands
B) Frowitz. B.H.; Varadi, A.; Scheraga, H.A.
R) BOWNITZ. B.H.; Varadi, A.; Scheraga, H.A.
R) Froc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984
A) Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374
A) Reference number: A94006; MUID: 85014892
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A;Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG ins are contained in the core. Two three-chain coiled coils emerge from this core and co
A;Title: Identification of proteins associated with apolipoprotein A-1-containing lipopz
A;Reference number: A54223; MUID:94162201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ger) and between alpha chains (weaker) of different monomers. C;Comment: All fibrinogen chains are synthesized in the liver. C;Comment: The two forms of gamma chain, A and B (see PIR:FGHUGB), arise by alternate spintron, which makes this chain different from the gamma-B chain at positions 434-437 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: hementin, a protease from Haementeria ghilianii, the giant South American leech, C; Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave ization sites responsible for the formation of the soft clot.

C; Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A37117; MUID:90337977
A;Contents: annotation; hementin cleavage site
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A;Cross_references: GDB:119132; OMIM:134850
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A; Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in A; Pathway: blood coagulation
C; Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C; Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote
E; 1-26/Domain: signal sequence #status predicted <SIG>Filomain: calcium binding #status predicted <CAB>Filomain: calcium for #status experimental <Filomain: interchain (to gamma-35) #status experimental <Filomain: interchain (to alpha-180) #status experimental <Filomain: interchain (to alpha-180) #status experimental <Filomain: interchain (to alpha-180) #status experimental <Filomain: interchain (to abeta-227) #status experimental <Filomain: interchain (to alpha-180) #status experimental <Filomain: interchain (to alpha-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;424/Cross-link: isopeptide (Gln) (interchain to gamma-432-Lys) #status experimental F;432/Cross-link: isopeptide (Lys) (interchain to gamma-424-Gln) #status experimental
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A;Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near t
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C; Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
C; Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
C; Accession: A90494; A92448; A90453; A28203; B28203; I37390; A03126
R; Rixon, M.W.; Chung, D.W.; Davie, E.W.
B; Correction of the game for the gamma chain of human fibrinogen.
A; Title: Nucleotide sequence of the game for the gamma chain of human fibrinogen.
A; Reference number: A90494; WUID: 85252774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 IHLLTKSKEM--ILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNY-NGTAGDAL-- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 -----RESRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYY 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 KP-----BIYUSRKMLE-EIMKYEASILTHDSSIRYLQ-----EIYUSNN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 DPGGNGGNGAETAEDSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 VDNKVANLTVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 HRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE----REFWLGNDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 QGGTYSKASTPNGYDNGIIWATW-------KTRWYSMKKTTWKIIPFN 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibrinogen gamma-B chain precursor - human
N;Alternate names: coagulation factor I; fibrinogen gamma-55 chain
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101 KP----NMIDAATLKSRKMLE-EIMKYEASILTHDSSIRYLQ--
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A;Residues: 1-36 <COT1>
A;Accession: B03124
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Matches 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Molecule type: protein
A.Residues: 433-453 <FR2>
R.Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
R.Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
R.Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
BNA Seq. 1, 419-422, 1991
A.Title: Polymorphism of the human gamma chain fibrinogen gene.
A.Reference number: 137390; MUID:92119334
A.Accession: 137390
A.Status: translated from GB/EMBL/DDBJ
A.Accession: 137390
A.Status: translated from GB/EMBL/DDBJ
A.Residues: 75-286 <RES>
A.Residues: 75-286 <RES>
A.Residues: 75-286 <RES>
A.Cross-references: EMBL.X51473; NID:931410; PIDN:CAA35837.1; PID:9930064
C.Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate splantron, which makes this chain different from the gamma-B chain at positions 434-437 and C.Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plase C.Genetics:
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A; Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C; Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG
ins are contained in the core. Two three-chain coiled coils emerge from this core and co
                                                                                                                                                                                                                                                                                         of a human fibrinogen gamma-chain variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the gamma-chain
                                                                          A; Molecule type: DNA
A; Residues: 286-453 <FOR>
R; Wolfenstein-Trodel, C.; Mosesson, M.W.
B; Wolfenstein-Trodel, C.; Mosesson, M.W.
B; Wolfenstein-Trodel, C.; Mosesson, M.W.
B; Title: Carboxy terminal amino acid sequence of a human fibrinogen gamma-chain val
A; Reference number: A90453; MUID: 82068993
A; Reference number: A90453; MUID: 82068993
A; Molecule type: protein
A; Residues: 411-434, 'Y', 436-440, 'Z', 444, 'B', 446-447, 'R', 449, 'ZBB', 453 <WOLD:
R; Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A; Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain constitution A28203
A; Molecule type: protein
A; Residues: 433-449 <FRA>
A; Molecule type: protein
A; Residues: A3203-449 <FRA>
A; Molecule type: protein
A; Residues: A3203-449 <FRA>
A; Molecule type: protein
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A, Cross-references: GDB:119132; OMIM:134850
number: A92448; MUID:85030379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity, 33.09
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from the distal domain nodes.
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C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu C;Keywords: blood coagulation; glycoprotein; sulfoprotein F;1-36/Product: fibrinopeptide B #status experimental <FPB>F;37-479/Product: fibrin beta chain #status experimental <MAT>F;90-219/Domain: fibrinogen disulfide ring homology <FDR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NyContains: fibrinopeptide B
NyContains: fibrinopeptide B
C;Species: Petromyzon marinos (sea lamprey)
C;Species: Petromyzon marinos (sea lamprey)
C;Date: 25-Oct-1887 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C;Accession: A25052; A03124; B03124
R;Bohonus, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
Bjiochemistry 25, 6512-6516, 1986
A;Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A;Reference number: A25052; MUID:87076582
                                                                                            --EIYNSNN---- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 PQEAQKAIRDEGG-C--MLPESDLGVICPTGCELREELLKQRDPVRYKISMLKQNLTYFI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 LQADDHRDPGGNGGNGAETAEDS-----RVQELESQVNKLSSELKNAKDQIQGLQGRLET 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 PARLEGSGRCEGSQCPFQLTLPTLTIQLPRQLGSMEEVLKEVRTLKEAVDSLKKSCQDCK 98
                                                                                                                                                                                                                       -----RESRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYY
                                                         166 VDNKVANLTVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 FDFGDDPSDKF - - FTSHNGMQFSTWDNDNKF - EGNCAEQDGSGWWMNKCHAGHLNGVYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- RMASDSNTLKQNVQTLRRRLNSRSSTHVNAQKEI---- ENRYKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --VOHLIY
                                                                                                                                                                                 226 HRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE----REFWLGNDK
                                                                                                                                                                                                                                                                                                          IHLLTKSKEM--ILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNY-NGTAGDAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:229-477/Domain: fibrinogen beta/gamma homology <FBG>F:13/Binding site: sulfate (Tyr) (covalent) #status experimental F:27/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 QGGTYSKASTPNGYDNGIIWATW------KTRWYSWKKTTMKIIPFN 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 H-----QKYKGVRNGIFWGTWPGINQAQPGGYKS---SFKQAKMMIRPKN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 LHLVNMNNIENYVDNKVANLTVVVNSLDGKCSK----CPSQEHMQSQP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.1%; Score 470.5; DB 2; 30.5%; Pred. No. 4.1e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibrinogen beta chain - sea lamprey (fragments)
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C; Species: Mus musculus (house mouse)
C; Species: Musculus (boundary)
C; Accession: JC5980
R; Fujimori, Y; Harumiya, S.; Fukumoto, Y; Miura, Y.; Yaqasaki, K.; Tachikawa, H.; F
Biochem. Biophys. Res. Commun. 244, 796-800, 1998
A; Title: Molecular cloning and characterization of mouse ficolin-A.
A; Reference number: JC5980; MUID:98205801
A; Reference number: JC5980
A; Residues: 1-334 <FUJ>
A; Residues: 1-334 <FUJ>
A; Residues: 1-334 <FUJ>
A; Residues: 1-344 <FUJ>
A; Residues: 1-354 <FUJ>
C; Comment: This protein consists of both collagen- and fibrinogen- like domains.
C; Comment: This protein consists of both collagen- and fibrinogen- like domains.
C; Superfamily: fibrinogen beta/gamma homology
F; 1-21/Domain: signal sequence #status predicted <COL>
F; 123-334/Domain: fibrinogen beta/gamma homology <FROS>
F; 123-334/Domain: fibrinogen beta/gamma homology <FROS>
                                                                                                                                                                                                                                                                                           cucumber (Parastichopus parvimensis)
                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: A35084
R; Xu, X.: Doolittle, R.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 2097-2101, 1990
A; Title: Presence of a vertebrate fibrinogen-like sequence in an echinoderm. A; Reference number: A35084; MUID: 90192754
A; Accession: A35084
                                                                                                                                                                                                                                                                                                                                                              C;Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 LGNHYYAKYNKFRIGDSFSEYLLVLGAYSGTAGDSLAY----HNTMRFSTYDNDNDVY- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 CPSQ-EHMQSQPVQHLIYKDCSDHYVLGRRS-----SGAYRVTPDHRNSSFEVYCDMETM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 CPKRISHSPEYP-----RDCYD--ILQSCSGQSPPSGQYYIQPDGGN-LIKVYCDMETD 106
397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEMILRIDLEDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGNCGLYYSSG---WWFDSCLSANLNGKYYHQKYKGVRNGIFWGTWPGINQAQPGGYKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 SINCASHSSYGRGAWWYKSCLLSNLNGQYY--DYSGAPS-IYWSYLPGDNDQIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 282;
348 -DGNCAEQVGIGWWMNKCHAGHLNGVYYQGGTYSKTSTPNGYDNGIIWATW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M31326; NID:g161164; PID:g161165
C;Superfamily: fibrinogen beta/gamma homology
F;67-280/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 19.8%; Score 463.5; Best Local Similarity 42.6%; Pred. No. 6.5e Matches 106; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                  - sea
                                                                                                                                                                                                                                                                                           fibrinogen-related protein A precursor
                                                                                                                                                                                                                                                                                                                             C; Species: Parastichopus parvimensis
                                                                                                        --KSRWYSMKKTTMKIIPLN 415
                                                                GYKS---SFKQAKMMIRPKN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-282 <XUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 FKQAKMMIR 426
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R; Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 6397, 1989
A; Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibrinc
A; Reference number: S05313; WUID: 8936676
A; Accession: S05313
A; Molecule type: mRNA
A; Residues: 1-444 < SBC>
A; Molecule type: mRNA
A; Residues: 1-444 < CBC>
A; Accession: S05313
A; Molecule type: mRNA
A; Residues: 1-444 < CBC>
A; Accession: S05313
A; Molecule type: mRNA
A; Residues: 1-444 < CBC>
A; Cross-references: EMBL:X1556; NID: 9349; PIDN:CAA33562.1; PID: 9350
A; Cross-references: EMBL:X1556; NID: 936676
A; Cross-references: EMBL:X1556; NID: 9349; PIDN:CAA33562.1; PID: 9350
A; Cross-references: EMBL:X1556; NID: 9349; PID: 9349; PID: 94444
A; Cross-references: EMBL:X1556; NID: 9349; PID: 94444
A; Cross-references: PID: 944444
A; Cross-references: PID: 94444
A; Cross-references: PID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Bos primigenius taurus (cattle)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
C;Accession: S05313
                                                                86 AVDSLKKSCQDCKLQADDHRDPGGNGGNGAETAEDSRVQELESQVNKLSSELKNAKDQIQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLQGRLETLHLVNMNNI----ENYVDN--KVANLTVVVNSLDGKCSKCPSQEHMQSQPVQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIM-KXETLISTHESTIRFLQEVYNSNSQKIVNLRDKVVQLEANCQE-PCQDTVK---IH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- HOKYKGVRNGIFWGTWPGINQAQPG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 PSGNCGLYYSSGWWFDSCLSANLNGKYYH-----QKYKGVRNGIFWGTWPGINQAQPG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 SACLAYVATRDNCCILDERFGSYCPTTCGIADFLNNYQTSVDKDLRTLEGILYQVENKTS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 AACPARLEGSGRC-----EGSQCPFQL----TLPTLTIQLPRQLGSMEEVLKEVRTLKE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTR
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                          KDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKD
                                                                                                                                                           YKAGFG------NLEREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQF
                                                                                                                                                                                                                                                                                           313 YVANEFLKYRLHIGNYNGTAGDALRFSRHY-----NHDLRFFTTPDRDNDRY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
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Pred. No. 7.7e-26;
3; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                    360 PSGNCGLYYSSGWWFDSCLSANLNGKYY----
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Conservative 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibrinogen gamma-B chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 GYKSSFKQAKMMIRPK 428
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464 WY--SMRQMAMKLRPK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Best Local Simi
Matches 138;
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A; Accession: A94309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibrinogen beta chain precursor - human
N.Alternate names: coagulation factor I
N.Contains: fibrinopeptide B
N.Contains: fibrinopeptide B
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Apr.1984 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C.Accession: B43568; A90469; B90469; I37389; A94433; A90437; A94309; G54223; A03121; B37
R.Chung, D.W.; Harris, J.E.; Darle, E.W.
AV. Exp. McB Biol. 281, 39-48, 1990
A.Title: Nucleotide sequences of the three genes coding for human fibrinogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Wolecule type: DNA

A; Residues: 9-191, [P. 193-491 <CHU>

R; Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.

Biochemistry 22, 3244-3250, 1983

A; Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribonu

A; Reference number: A90469; MUID:83283433
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A;Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene. A;Reference number: 137389; MUID:87146483
A;Accession: 137389
A;Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-38 < HUB>
A; Cross-references: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
A; Cross-references: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
B; Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
In Protides of the Biological Fluids, Proc. 28th Collog., Peeters, H., ed., pp.51-56, PA; Title: Human fibringen: sequence, sulfur bridges, glycosylation and some structural
                                                                   7;
                                                                                                                                                                                                                                                        DYKAGFGNLEREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYR 322
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                 204 KDCSDHYVLGRRSSGAYRV-TPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWK 262
                                                                                                                                                                    182 SYKRGFGNLGTEFWLGNDYLHLLTANGNQELRVDLQDFQGKGSYAKYSSFQVSEEQEKYK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 9-191,'A',193-491 <CH2>
A;Cross-references: GB:J00129; NID:g182429; PIDN:AAA52429.1; PID:g182430
                                                                                                                                                                                                                                                                                                                                                                                LHIGNY-NGTAGDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSAN
                                                                   18;
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         Length 334;
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R;Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 LNGKYYHQKYKGVRNGIFWGTWPGINQAQPGGYKSSFKQAKMMIR 426
   ; Score 463; DB 2; L
; Pred. No. 8.8e-26;
30; Mismatches 78;
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19.8%;
44.0%;
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                                                                   99; Conservative
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Residues: 1-38 <CH1>
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A WILLIE Disullide bridges in NR 2-terminal part of human fibrinogen.

A Wordstoners: disulfide brodges in NR 2-terminal part of human fibrinogen.

A Wordstoners: disulfide brodges in NR 12-terminal part of human fibrinogen.

A Wordstoners: disulfide brodges in NR 12-terminal part of the A Wordstoners: disulfide brodges with the A Wordstoners and A Wordstoners and A Wordstoners.

B Wondstoners: disulfide brodges with the A Wordstoners are a wordstoners.

B Wondstoners: distriction of proteins associated with apolipoprotein A T-containing lip A Wordstoners.

A Wordstoners: distriction of proteins associated with apolipoprotein A T-containing lip A Wordstoners.

A Wordstoners: distriction of Wordstoners associated with apolipoprotein A T-containing lip A Wordstoners.

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A Wordstoners: distriction of Wordstoners and Wordstoners.

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R;Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981 A;Title: Characterization of a cDNA clone coding f A;Reference number: A37513; MUID:81199473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 -SMKKMSMKIRP 463
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Best Local Similarity
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A; Molecule type: protein
R; Mesidues: 5-21 GsJO>
R; Martinelli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S Arch. Biochem. Biophys. 192, 27-32, 1979
Arch. Biochem. Biophys. 192, 27-32, 1979
A; Tittle: Amino acid sequences of portions of the alpha and beta chains of bovine fibrind A; Reference number: A37507; MUID:79164394
A; Accession: B37507
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N;Contains: fibrinopeptide B
C;Species: Bos primigenius taurus (cattle)
C;Decies: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996
C;Decession: A03122; B03117; B37507; A37513; S02443
R;Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A;Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide
A;Reference number: A03122
                                                                                                                                                                                                                                               13;
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                                                                                                                                                                                                                                                                                                                        92 KSCQDCKLQADDHRDPGGNGGNGAETAEDS-------RVQELESQVNKLSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKV----ANLTVVVNSLDGKCSKCPSQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETMGGGWTVLQARLDGSTNFTREWKDYKAGFGN------LEREFWLGNDKIHLL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                NNVEAV------SQTSSSSFQYMYLLKDLWQKRQKQVKDNENVVNEYSS 174
                                                                                                                                                                                                                                                                                        32 ASAQAACPARLEGSGRCEGSQCPFQLTLPTLT1QLPRQLGSMEEVLKEVRTLKEAVDSLK 91
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F;106/Disulfide bonds: interchain (to alpha-68) #status experimental F;110/Disulfide bonds: interchain (to gamma-45) #status experimental F;227/Disulfide bonds: interchain (to alpha-184) #status experimental F;227/Disulfide bonds: interchain (to alpha-184) #status experimental F;227/Disulfide bonds: interchain (to gamma-161) #status experimental F;331-316,241-270,424-437/Disulfide bonds: #status experimental F;394/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                            ; Score 463; DB 1; Length 491;
; Pred. No. 1.4e-25;
60; Mismatches 151; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 TWDMAKHGTDDGVVWMNWKG-----SWY--SMRKMSMKIRP 486
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A; Residues: 1-4 (BLO:
R; Sigoquist, J: Blomback, B.; Wallen,
Ark: Kemi 16, 425-436, 1960
                                                                                                                                                                                            19.8%;
28.4%;
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Matches 131;
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restrictin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JH6675; PS0385; S23254
R;Noerenberg, U.; Wille, H.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
Neuron 8, 849-863, 1992
A;Title: The chicken neural extracellular matrix molecule restrictin: similarity with
                                                                                                                                                                                                                                                                                                                                                                                               A. Mocession: 502443
A. Molecule type: protein
A. Mesidues: 373-374 cMED>
C. Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopept
C. Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (C. Superfamily: fibrinogen beta chain; fibrinogen beta/damma homology; fibrinogen disulfide ring homology cFDR>
F. 76-205/Domain: fibrinogen beta/gamma homology cFDR>
F. 17-464/Domain: fibrinogen beta/gamma homology cFDR>
F. Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F. Affinding site: sulfate (Tyr) (covalent) #status experimental
F. 371/Binding site: carbohydrate (Asn) (covalent) #status predicted
F. 372-373/Cleavage site: Arg-1hr (plasmin) #status experimental
                                                                      A; Accession: A37513
A; Molecule type: mRNA
A; Residues: 44.468 < CHU>
B; Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FBBS Lett. 232, 56-60, 1988
A; Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads
A; Reference number: S02443; MUID:88211875
for the beta chain of bovine fibrino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 NEFLKYRLHIGNYNGTAGDAL-----RFSRHYNHDLRFFTTPDRDNDRY----PSG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 NCGLYYSSGWWFDSCLSANLNGKYY-----HQKYKGVRNGIFWGTWPGINQAQPGGYK 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 GSQCPFQLTLPTLTIQLPRQLGSMEEVLKEVRTLKEAVDSLKKSCQDCKLQADDHRDPGG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 QCSKEDGGGWWYNRCHAANPNGRYYWGGAYTWDMAKHGTDDGVVWMNWQG-----SWY- 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AEDSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- ETVKNNIPTKLRVLRSILENLRSKIQKLESDVSTQMEYCRTPCTVTCNIPVVSGKECE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 NMNNIENYVDNKVANLTVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 GVLCPTGCKLQDTLVRQER-----PIRKSIEDLRNTVDSVSRT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.6%; Score 458; DB 1; 28.5%; Pred. No. 3.1e-25;
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                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 579-586;827-840 (NOE1>
C; Comment: This protein is a neural extracellular matrix protein implicated in neural cc C; Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibrinogen typ C; Reywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycoprot F; 1-33/Domain: signal sequence #status predicted <SIG>
F; 34-1353/Product: restrictin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:1035-1115/Domain: fibronectin type III repeat homology <FN9>
F:1130-1338/Domain: fibrinogen beta/gamma homology <FBGO
F:1120-1286/Region: calcium binding #status predicted
F:53,197,277,391,469,580,734,790,960,1031,1041,1256,1342/Binding site: carbohydrate (Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Cross-references: GB:MS8569; NID:q182406; PID:q182407
A)Note: neither the complete nucleic acid sequence nor the complete translation are show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the human fibrinogen alpha subunit: a nove
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R;Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, Biochemistry 31, 11968-11972, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYKAGFGNLEREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 KDCSDHYVLGRRSSGAYRVTPD-HRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHIGNYNGTAGDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANL 382
                                                                            A;Residues: Î-1353 <NOE>
A;Cross-references: GB:X64649; NID:g63613; PIDN:CAA45920.1; PID:g63614
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.4%; Score 454.5; DB 1; Length 1353; 41.0%; Pred. No. 2.1e-24; Live 33; Mismatches 83; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1304 NGKYGESRHS---QGINWYHWK-----GHEFSIPFVEMKMRPYNHR 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 NGKYYHQKYKGVRNGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNFK 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fibrinogen alpha chain precursor, extended splice form - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;949-1027/Domain: fibronectin type III repeat homology <FN8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat
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A; Reference number: JH0675; MUID:92265298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A44234; MUID:93090725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r;324-405/Domain: fibronectin type III F;592-5676/Domain: fibronectin type III F;592-676/Domain: fibronectin type III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                       F;203-229/Domain: EGF homology <EG1>F;244-260/Domain: EGF homology <EG2>F;26-291/Domain: EGF homology <EG3>F;26-322/Domain: EGF homology <EG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94; Conservative
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A; Molecule type: mRNA; DNA
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                                                      A; Molecule type: mRNA
                                                                                                                                                              A; Accession: PS0385
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F;324-405/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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Note: sequence extracted from NCBI backbone (NCBIP:119917)
C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cle ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stab ger) and between alpha chains (weeker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: See PIR:FGHUA for the major splice form. It is not known whether this form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 4928-4928
A; Introns: 18/3; 60/3; 122/1; 171/2
A;Note: the list of introns is incomplete
A;Complex: The fibrinogen molecule is a hexamer containing two sets of three nonident ntained in the core. Two three-chain coiled coils emerge from this core and connect i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Pathway: blood coagulation
C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
C; Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprot
F; 1-19/Domain: signal sequence #status predicted csls
F; 20-863/Product: fibrinogen alpha chain, extended splice form #status predicted cMAT
F; 20-35/Product: fibrinopeptide A #status experimental cAPT>
F; 30-863/Product: fibrinopeptide A #status experimental cAPT>
F; 57-185/Domain: fibrinogen disulfide ring homology cPDR>
F; 591-593/Region: cell attachment (R-G-D) motif
F; 629-863/Domain: fibrinogen beta/gamma homology cFDG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #status pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 TLYALYDQFYVANEFLKYRLHIGNYNGTAGDAL-----RFSRHYNHDLRFFTTPDRDND 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 HMQSQPVQHLIYKDCSDHYVL----GRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F.22.460/Binding site: phosphate (Ser) (covalent) #status experimental F.35.460/Binding site: phosphate (Ser) (covalent) #status experimental F.35.36/Cleavage site: Arg-Gly (thrombin) #status experimental F.47/Disulfide bonds: interchain (to alpha-47) #status experimental F.56/Disulfide bonds: interchain (to beta-95) #status experimental F.64/Disulfide bonds: interchain (to pera-16) #status experimental F.180/Disulfide bonds: interchain (to gamma-165) #status experimental F.180/Disulfide bonds: interchain (to beta-223) #status experimental F.181/Disulfide bonds: interchain (to beta-223) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 RYPSGNCGLYYSSGWWFDSCLSANLNGKYY-----HQKYKGVRNGIFWGTWPGINQ
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Pred. No. 1.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GDB:119129; OMIM:134820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: FGA
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-----SLRAVRMKIRP 862

Job time: 157 sec

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February 27, 2001, 12:48:38; Search time 30.15 Seconds (without alignments) 489.941 Million cell updates/sec
                                                                                                                                                                                                                                                                                                               2340
1 MRLPGWLWLSSAVLAACRAV......GYKSSFKQAKMMIRPKNFKP 432
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/SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp/AA1997.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/geneseg/genesegp/AA1998.DAT:*/SIDS1/gcgdata/geneseg/genesegp/AA1999.DAT:*/SIDS1/gcgdata/geneseg//genesegp/AA2000.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268485 seqs, 34193795 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                                                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                     US-09-442-143-4
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                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                          OM protein
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                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Mouse prothrombina	Human prothrombina	Amino acid sequenc	. Rat hepatic parenc	Human TIE-2 ligand	Human TIE-2 ligand	Human TIE-2 ligand	Human angiopoletin	Human anglopoletin	Amino acid sequenc	Hepatocyte prolife	Hepatocyte prolife
SUMMARIES	W88236	W88235	W47529	R65759	W01411	R94605	W47532	X78903	X78906	W47528	R94317	R94316
DB	20	20	19	15	17	17	19	21	21	19	17	17
% Query Match Length DB	432	439	499	314	496	496	496	496	496	498	312	312
% Query Match	100.0	79.2	23.0	22.8	22.8	22.8	22.8	22.8	22.8	22.6	22.4	22.3
Score	2340	1853.5	537.5	533.5	533.5	533.5	533.5	533,5	533.5	528	524	523
Result No.		~	٣	4	5	9	7	80	σ	10	11	12

98WO-CA00475. 97US-0061684.

15-MAY-1998; 10-OCT-1997;

R65760 Y23736 Y23736 Y23736 Y2373736 Y278904 Y278904 Y278904 Y278904 W47527 W47527 Y28902
11.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0
3312 4666666666666666666666666666666666666
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44 44 44 44 44 44 44 44 44 44 44 44 44
E 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

Prothrombinase, Fg12; mouse; immune coagulation; antibody; inhibitor; infection; graft rejection; glomerulonephritis; cancer; gastrointestinal disease; foetal loss; therapy; vaccine. /note= "Asn is N-glycosylated" 323..325 hote= "Asn is N-glycosylated" 213..439 /note= "fibrinogen related domain" 228..231 /note= "Asn is N-glycosylated" /label= Asn is N-glycosylated Location/Qualifiers 172..174 Mouse prothrombinase Fg12 protein. RESULT 1 W88236 ID W88236 standard; Protein; 432 AA. 15-MAR-1999 (first entry) /note= "A 256..259 Key Modified-site Modified-site Modified-site Modified-site 409851335-A1 19-NOV-1998 W88236; Mus sp. Domain Ä.

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Prothrombinase; hfgl2; Fgl2; human; immune coagulation; antibody; inhibitor; infection; graft rejection; glomerulonephritis; cancer; gastrointestinal disease; foetal loss; therapy; vaccine.
                                                                    Human prothrombinase Fg12 protein.
  W88235 standard; Protein; 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-059687/05.
N-PSDB; V84139.
                                                                                                                                                                       Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                        (LEVY/) LEVY
                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 15-MAY-1998;
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                                             15-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             foetal loss
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                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TLTIQLPRQLGSMEEVLKEVRTLKEAVDSLKKSCQDCKLQADDHRDPGGNGGNGAETAED 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKVANLTVVVVNSL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTPDRDNDRYP 360
                                                                                                                                                                  This is the amino acid sequence of mouse prothrombinase Fgl2, as predicted from fgl2 DNA (see V84140). Fgl2 is a 70 kDa transmembrane serine protease that has immune procoagulant activity. The human Fgl2 amino acid sequence is given in W88236. The invention provides a method for inhibiting immune coagulation by inhibiting the activity or expression of Fgl2. The method can be used in vivo to treat a condition which requires a reduction in immune coagulation such as bacterial and viral infections, cancer, glomerulonephritis, a number of gastrointestinal diseases, allograft and xenograft rejection and foetal loss. An Fgl2-specific
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRLPGWLWLSSAVLAACRAVEEHNLTEGLEDASAQAACPARLEGSGRCEGSQCPFQLTLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating immune coagulation - by using Fg12 antibodies and compounds, used to treat conditions including graft rejection and foetal loss
                                                                                                                                                                                                                                                                                 antibody, an Fg12 antisense oligonuclectide, or a substance that affects prothrombinase activity of a Fg12 protein may be used to treat a condition requiring a reduction in procoagulant activity. A vaccine containing an Fg12 protein or peptide is used for prevention of graft rejection or foetal loss (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 2340; DB 20; Length 432; 100.0%; Pred. No. 2.2e-199; Ive 0; Mismatches 0; Indels 0;
                                                                                                                                               Claim 8; Page 70-71; 105pp; English.
97US-0046537.
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Matches 432; Conservative
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                                                                                                                                                                                                                                                                                                                                                       432 AA;
                      (LEVY/) LEVY G.
                                                                              N-PSDB; V84140.
15-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                             Levy G;
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"fibrinogen related domain"

/note= "f

336..337 ..439

/note= /note= /note= "epitope (Claim 4)"

98WO-CA00475

97US-0046537

/note= "Asn is N-glycosylated" 262..265 "Asn is N-glycosylated" "Asn is N-glycosylated"

/label= Asn is N-glycosylated

Location/Qualifiers

..183 235..238

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4
                                                                                                                                                                                                                                                                                            predicted from highl DNA (see V84139). Fgll is a 70 kDa transmembrane serine protease that has immune procoagulant activity. The invention provides a method for inhibiting immune coagulation by inhibiting the activity or expression of Fgll. The method can be used in vivo to treat a condition which requires a reduction in immune coagulation such as bacterial and viral infections, cancer, glomerulonephritis, a number of gastrointestinal diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allograft and xenograft rejection and foetal loss. An F912-specific antibody, an F912 antisense oligonucleotide, or a substance that affects prothrombinase activity of a F912 protein may be used to treat a condition requiring a reduction in procoagulant activity. A vaccine containing an F912 protein or peptide is used for prevention of graft rejection or foetal loss (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Gaps
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Modulating immune coagulation - by using \mathrm{Fg12} antibodies and compounds, used to treat conditions including graft rejection and
                                                                                                                                                                                                                                                             This is the amino acid sequence of human prothrombinase Fgl2, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 439;
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                                                                                                                                                                           Claim 8; Page 66-67; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.2%
Best Local Similarity 77.7%
Matches' 341; Conservative
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19;
useful for blocking blood vessel growth, promoting neovascularisation, promoting the growth or differentiation of a cell expressing the TIE receptor, blocking the growth or differentiation of a cell expressing the TIE receptor and for attenuating or preventing tumour growth in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: | :: : | :: : | | | :||| :| ::|:||
emveiggnavgngtavmieigtnlln--gtaegtrkltdveagvlngttrlelgllehsl 168
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169 stnklekgildgtseinklgdknsflekkvlamedkhiiqlgsikeekdglgvlvskqns 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463
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                                                                                                                                                                                                                                                                                                                                        --NKLSSELKNAKDOIOGLOGR------LETLHLVNMNNIENYVDN---KVANLTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LWLSSAVLAACRAVEEHNLTEGLEDASAQAACPARLEGSG----RCEGSQCPFQLTLP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 YNGTAGDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCQDCKLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV------
                                                                                                                                                                                                                   Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatic parenchymal cell growth factor; HPGF; liver diseases;
                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                             Score 537.5; DB 19;
Pred. No. 2.2e-39;
.....trhes 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 VVNSLDGKC----SKCPSQEHMQSQPVQHLI-----
                                                                                                                                                                                                                                                                                                                                                                                                         ---TLTIQLPRQLGSMEEVLKEVRTLKEAV--
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/label= sig_peptide
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                                                                                                                                                                                                                   23.0%;
28.4%;
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                                                                                                                                                                                                                                                                 Conservative
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us-09-442-143-4.rag

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N-PSDB; T44321
                                           06-OCT-1995;
06-APR-1995;
                      05-APR-1996;
  10-0CT-1996.
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db
                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                              Q77818 encodes R65759 rat hepatic parenchymal cell growth factor (HPCF). The protein or the N-terminal peptide (R65758) may be used in the diagnosis and treatment of liver diseases, such as liver cancer and
                                                                                                                                                                                                                                                                                                                                                      176 VVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYC 235
                                                                                                                                                                                                                                                                                                                                                                   mkfstrdrdndny-ngncaeeeqsgwwfnrchsanlngyyyggpyraetdngvvwytw-- 290
                                                                                                                                                                                                                                                                                                             119 EDSRVQE---LESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKVANLTV 175
                                                                                                                                                                                                                                                                                                                                                                                                  DMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLER---EFWLGNDKIHLLTKSKEMI 292
                                                                                                                                                                                                                                                                                                                                                                                                                     dmsd-gggwtviqrrsdgsenfnrgwndyengfgnfvqsngeywlgnkninlltmqqdyt 173
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIE-2 ligand 2; tyrosine kinase with Ig and EGF homology domain; receptor; antagonist; neovascularisation; wound healing; ischaemia; leukopaenia; thrombocytopaenia; anaemia; angiogenesis; tumour; atherosclerosis; inflammation; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                           LRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRH-----YNHDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 RFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKG-VRNGIFWGTWPG
                                                                                                                Hepatic parenchymal cell growth promoter peptide - is isolated from human or animal liver cell or produced by recombinant techniques and used for therapy of liver diseases
                                                                                                                                                                                                                                                                      Length 314;
                                                                                                                                                                                                                                                                                          Indels
                                                                Yoshimura H;
                                                                                                                                                                                                                                                                      DB 15;
                                                                                                                                                                                                                                                                  22.8%; Score 533.5; DB 15; 38.2%; Pred. No. 2.5e-39; ive 46; Mismatches 103;
                                                                Shindo S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          406 INQAQPGGYKSSFKQAKMMIRPKNFKP 432
                                                                                                                                                          Claim 3; Page 34; 47pp; Japanese
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                                                             Matsuki Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W01411 standard; Protein; 496
94WO-JP00455
                     93JP-0063905
                                       (TAIS ) TAISHO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                               Best_Local Similarity 38.2
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TIE-2 ligand 2.
                                                                                WPI; 1994-316940/39.
                                                               Hanada K, Hara H,
                                                                                                                                                                                                                                      314 AA;
                                                                                              N-PSDB; Q77818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9631598-A1
                     23-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                      Sequence
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53 crsssspyvsnavgrdapleyddsvgrlqvlenimenntqwlmklenyiqdnmkkemvei 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 REFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 GDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYK 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 CEGSQCPF----QLTLPTLTIQLPRQLGSMEEVLKE----VRTLKEAV-DSLKKSCQDC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human TIE-2 (tyrosine kinase with Ig and EGF homology domains) ligand 2 (W01411) is a ligand that binds the TIE-2 receptor. Its amino acid sequence was deduced from a cDNA clone (T44321) derived from human foetal lung cells. TIE-2 ligand 2 is a receptor antagonist useful for blocking blood vessel growth, for tumour therapy and for treating a proliferative disorder of a blood forming organ. It can be obtd. from natural sources or expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: : :| || : :: |
171 ekqildqtseinklqdknsflekkvlamedkhiiqlqsikeekdqlqvlvskqnsiieel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 GRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17; Length 496;
                                                                                                                                                                                                                                                                                                                                                                         TIE-2 agonists and antagonists and related DNA - useful for promoting or blocking neovascularisation, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                      Jones 1
GD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 KLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.8%; Score 533.5; DB 17; 29.4%; Pred. No. 4.9e-39; Live 80; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 GVR-NGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNF 430
                                                                                                                                                                                                Goldfarb M,
Yancopoulos
                                                                                                                                                                                                   Aldrich TH, Bruno J, Davis S,
Maisonpierre PC, Radziejewski C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R94605 standard; Protein; 496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Fig 6; 113pp; English.
                                                        95WO-US12935.
95US-0418595.
                                                                                                                                              (REGE-) REGENERON PHARM INC.
96WO-US04806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in transformed host cells.
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Matches 135; Conservative
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DGKC-----SKCPSQEHMQSQPVQHLI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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02-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R94605 is a human TIE-2 (hTIE-2) ligand 2 derived from a pBluescript KS clone. hTIE-2 ligand DNAs of the invention are recombinant versions of the native ligand coding sequences and may be used to produce the ligands at a high yield. Antibodies and receptor bodies that bind to TIE-2 ligands may be used to inhibit angiogenesis and neovascularisation (e.g. associated with tumour development) and the TIE-2 ligands themselves are useful to promote neovascularisation and wound healing e.g. for treatment of ischamia. TIE-2 ligands are also useful to diabetes. Ligand bodies contg. TIE-2 ligands may also be useful for the delivery and targeting of growth factors, toxins etc. to sites where their presence is advantageous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 crsssspyvsnavgrdapleyddsvgrlgvlenimenntgwlmklenyigdnmkkemvel 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 KLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV---------NKL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSELKNAKDQIQGLQGR------LETLHLVNMNNIENYVDN---KVANLTVVVNSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                neovascularisation; tumour development; wound healing;
                                                                                                                                                TIE: tyrosine kinase with Ig and EGF homology domains; vector; recombinant; clone; diagnosis; ischaemia; thromboembolytic disease; atherosclerosis; inflammation; diabetes; ligand bodies; delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding TIE-2 ligand and related vectors - useful in diagnosis and treatment of neovascularisation, tumours, etc., or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 CEGSQCPF-----QLTLPTLTIQLPRQLGSMEEVLKE----VRTLKEAV-DSLKKSCQDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.8%; Score 533.5; DB 17; Length 29.4%; Pred. No. 4.9e-39; ive 80; Mismatches 153; Indels
                                                                                   Human TIE-2 ligand 2 derived from pBluescript KS clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goldfarb M, Jones PF;
Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aldrich TH, Bruno J, Davis S,
Maisonpierre PC, Radziejewski C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 6; 84pp; English.
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94US-0330261.
94US-0348492.
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95US-0373579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis and treatment of promote wound healing, etc.
                                          (first entry)
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Best Local Similarity
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                                                                                                                                Angiogenesis;
                                          28-OCT-1996
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                        WO9611269-A2
                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-1995;
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27-0CT-1994;
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                                                                                                                                                                                                                      targeting.
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This is the amino acid sequence of the human TIE-2 ligand 2, used in the method of the invention, involving the production of TIE-2 ligands which promote healing. The nucleic acids, vectors and host cells used in the method of the invention are useful for the recombinant production of the ligands. The ligands, etc. are useful for blocking blood vessel growth, promoting neovascularisation, promoting the growth or differentiation of a cell expressing the TIE receptor, blocking the growth or differentiation of a cell expressing the TIE receptor and for attenuating or preventing tumour growth in
--YKDCSDHYVL 212
                                                                                                                                                                                                                                                                                                                                                                                                                            Modified human TIE-2 receptor ligand(s) - useful for promoting wound
                                                                                                                             213 GRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE
                                                                                                                                                                 333 GDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYK
                                                              231 ekkivtatvnnsvlqkqqhdlmetvnnlltmmstsnsakdptvakeeqisfrdcaevfks
                                                                                                                                                                                                                                                       273 REFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric TIE ligand 2N1C1F; TIE-2 ligand; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 GVR-NGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNF 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 533.5; DB 19
Pred. No. 4.9e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TIE-2 ligand 2 from clone pBluescript KS.
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                                                                     SSELKNAKDQIQGLQGR-----LETLHLVNMNNIENYVDN---KVANLTVVVNSL 180
                                                                                                                                                                                       | ::||:| :| | | ghttngiytltfpnsteeikaycdmeaggggwtiiqrredgsvdfgrtwkeykvgfgnps 350
                                                                                                                                                                                                                               GDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYK 392
                                                                                                                                                                                                                                                                            gkissisqpgnd----fstkdgdndkcic-kcsqmltggwwfdacgpsnlngmyypqrqn 465
                                | | |: |: |::|| ;:| crsssspyvsnavgrdapleyddsvqrlqvlenimenntqwlmklenyiqdnmkkemvei 112
                                                                                                                                        ----YKDCSDHYVL 212
                                                                                                                                                          231 ekkivtatvnnsvlgkgghdlmetvnnlltmmstsnsakdptvakeegisfrdcaevfks 290
                   CEGSQCPF----QLTLPTLTIQLPRQLGSMEEVLKE----VRTLKEAV-DSLKKSCQDC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binding ligand for aminophospholipid used in the treatment of vascularised tumours, comprises targeting component and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiopoietin-2; Ang-2; vascular endothelial growth factor; tumour; vascularisation; angiogenesis; blood vessel maturation; malignant; benign; binding ligand; cancer; aminophospholipid.
                                                                                                                                                                             GRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE
                                                                                                             REFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTA
 91;
  Indels
 153;
                                                                                                                                                                                                                                                                                                393 GVR-NGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNF 430
                                                                                                                                                                                                                                                                                                             KLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV-
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Human angiopoletin-2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 257-259; 267pp; English.
                                                                                                                                       DGKC----SKCPSQEHMQSQPVQHLI-----
80;
                                                                                                                                                                                                                                                                                                                                                                   Y78903 standard; Protein; 496
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JAN-2000
Matches 135;
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                                                                                                                                                                                                                                                                                                                                                                                       Y78903;
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This sequence represents the human angiopoietin-2 (Ang-2) amino acid sequence. Ang-2 is a naturally occurring angiogenesis antagonist when vascular endothelial growth factor (VEGF) levels are low, and generally counteracts the blood vessel maturation and stability mediated by Ang-1. Ang-1 is a naturally occurring angiogenesis agonist, and is a maturation or stabilisation factor, converting immature vessels to mature vessels. Both Ang-1 and Ang-2 are useful in a therapeutic approach to the treatment of vascularised tumours. The invention relates to a binding ligand comprising a targeting agent that binds to an aminophospholipid, and specific markers accessible on the luminal surface of tumour blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; angiopoietin-2; Ang-2; aminophospholipid; vascularised tumour;
unconjugated anti-aminophospholipid antibody; tumour blood vessel marker;
cancer; treatment; angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                        vessels. The binding ligand induces coagulation (thrombosis) in tumour vasculature or causes tumour necrosis (possibly by cell- or complement-mediated cytotoxicity and/or apoptosis). The binding ligands are used to treat vascularised tumours, malignant or benign, in animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 KLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV-------NKL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 SSELKNAKDQIQGLQGR------LETLHLVNMNNIENYVDN---KVANLTVVVNSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 REFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 GDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYK 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 crsssspyvsnavgrdapleyddsvgrlqvlenimenntgwlmklenyiqdnmkkemvei 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 gkissisqpgnd----fstkdgdndkcic-kcsqmltggwwfdacgpsnlngmyypgrqn 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 CEGSQCPF----QLTLPTLTIQLPRQLGSMEEVLKE----VRTLKEAV-DSLKKSCQDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 GRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 135; Conservative 80; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human angiopoietin-2 (Ang-2) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 GVR-NGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNF 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 tnkfngikwyywkg----sgy--slkattmmirpadf 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 4.9e-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.8%; Score 533.5; 29.4%; Pred. No. 4.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 DGKC----SKCPSQEHMQSQPVQHLI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y78906 standard; Protein; 496 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             especially large tumours.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Best Local
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                                                                                            RESULT 10
W47528
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                                                                                                                                                                                                                                                                                                                                                                                                                    sequence. Ang. 2 is a naturally occurring angiogenesis antagonist when vascular endothelial growth factor (VEGF) levels are low, and generally counteracts the blood vessel maturation and stability mediated by Ang-1. Ang. 1 is a naturally occurring angiogenesis agonist, and is a maturation or stabilisation factor, converting immature vessels to mature vessels. Both Ang-1 and Ang-2 are useful in a therapeutic approach to the treatment of vascularised tumours. The invention relates to a composition comprising an anti-aminophospholipid antibody, or its antigen binding region. The composition is used to kill tumour vasculature endothelial calls. Aminophospholipids are stable and specific markers accessible on the luminal surface of tumour blood vessels. Ang-1 or Ang-2 may be used in the composition of the invention. The composition is used to treat malignant or benign vascularised tumours in animals, especially large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                  New composition for killing tumour vascular endothelial cells for treating solid tumours, comprises unconjugated anti-aminophospholipid antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | :: : | | | :||| :||| :|| :||| | gnavgngtavmieigtniln--qtaeqtrkltdveaqvlngttrlelgllehslstnkl 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ekkivtatvnnsvlqkqqhdlmetvnnlltmmstsnsakdptvakeeqisfrdcaevfks 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::||:| | | | ghttngiytltfpnsteeikaycdmeagggggwtiiqrredgsvdfgrtwkeykvgfgnps 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV------NKL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 SSELKNAKDQIQGLQGR-----LETLHLVNMNNIENYVDN---KVANLTVVVNSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYK 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human angiopoietin-2 (Ang-2) amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEGSQCPF----QLTLPTLTIQLPRQLGSMEEVLKE----VRTLKEAV-DSLKKSCQDC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGKC-----SKCPSQEHMQSQPVQHLI-------YKDCSDHYVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.8%; Score 533.5; DB 21; Length 29.4%; Pred. No. 4.9e-39; ive 80; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 223-224; 226pp; English.
                                                                       99WO-US15600
                                                                                                                            98US-0110608
                                                                                                             98US-0092672
                                                                                                                                                               (TEXA ) UNIV TEXAS SYSTEM.
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Matches 135; Conserv
                                                                                                                                                                                                     Ran S;
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WO200002584-A2.
                                                                                                                                                                                                                                                           N-PSDB; 292215
                                                                                                           13-JUL-1998;
02-DEC-1998;
                                                                       12-JUL-1999;
                                     20-JAN-2000
                                                                                                                                                                                                     Thorpe PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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This is the amino acid sequence of the chimeric TIE ligand INIC2F, used in the method of the invention, involving the production of TIE-2 ligands which promote healing. The nucleic acids, vectors and host calls used in the method of the invention are useful for the recombinant production of the ligands. The ligands, etc. are useful for blocking blood vessel growth, promoting neovascularisation, promoting the growth or differentiation of a cell expressing the receptor, blocking the growth or differentiation of a cell expressing the TIE receptor and for attenuating or preventing tumour growth in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              avgnhtatmleigtslisgtaegtrkltdvetgvlngtsrleigllenslstyklekgll 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KEAVDSLKKSCQDCKLQADDHRDPGGNGGR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 TAEDSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLH-LVNMNNIENYVDNKVANLTV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 VVNSLDGKCSK----CPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSF 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified human TIE-2 receptor ligand(s) - useful for promoting wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 AVEEHNL-----TEGLEDASAQAACPARLEGSGRCEGSQCPFQLTLPTL-TIQLPRQ-L 70
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                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of chimeric TIE ligand 1N1C2F (chimera 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric TIE ligand 1N1C2F; TIE-2 ligand; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 1.5e-38;
0; Mismatches 142;
393 GVR-NGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNF 430
                                                           466 tnkfngikwyywkg----sgy--slkattmmirpadf 496
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                                                                                                                                                                                                                          W47528 standard; Protein; 498 AA
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Conservative 70;
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
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312 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rat; probe; SR-alpha promoter;
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                                                                                :|:| |:| |:| | |:||: ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:
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ovary cell; CHO; hepatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    342 -YNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKG-VRNGIF 399
                                                                                    112 GNGAETAEDSRVQE--LESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNK 169
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                                                                                                            170 VANLTVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNS
                                                                                                                                                                                                                                                           287 KSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRH-----
                                          52;
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Query Match 22.4%; Score 524; DB 17; Best Local Similarity 37.8%; Pred. No. 1.7e-38; Matches 126; Conservative 41; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chinese hamster ovary cell; CHO; hepatitis.
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/note= "signal peptide"
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/note= "mature protein"
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N-PSDB; T13396.
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                  N-PSDB; Q77819
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        This is the amino acid sequence of a human hepatocyte proliferation substance (HPS). The gene encoding the HPS was isolated from a lambda-gt10 human cDNA library using a fragment of the corresp. rat gene as a probe (sequence not given in the specification). The human gene was cloned in plasmid pSCL to produce plasmid pSVLH which was subsequently recombined to produce plasmid pcDLH-dhfr in which the HPS gene is under control of the SR-alpha promoter. The splasmid is transformed into CHO cells to express the HPS protein. The HPS protein can be used to diagnose
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                                                                                                                                                                                                                     170 VANLTVVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNS 229
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                                                                                                                                                                                                                                                                                                                                          342 -YNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKG-VRNGIF 399
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                                                                                                                                                                                                                                                                                                               287 KSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRH----
                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ic parenchymal cell growth factor; HPGF; liver diseases;
cancer; cirrhosis.
                                                                                                                                        22.3%; Score 522; DB 17; Length 312; 37.5%; Pred. No. 2.5e-38;
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshimura H;
                                                                                                                                                            42; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human hepatic parenchymal cell growth factor
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                                                                                                                                                                                                                                                                                                                                                                                             Shindo S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..22
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R65760 standard; protein; 312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hara H, Matsuki Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TAIS ) TAISHO PHARM CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                            Conservative
                                                                                                                                                 Best_Local Similarity
Matches 125; Conser
                                                                                                           312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-1994;
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                                                                                      hepatitis
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liver ca
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                                                                                                                                                                077819 encodes R65760 rat hepatic parenchymal cell growth factor (HPGF). The protein or the N-terminal peptide (R65757) may be used in the diagnosis and treatment of liver diseases, such as liver cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dentvidlgs------krq----yadcseifndgyklsgfykikplqsla 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 -YNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKGVRN-GIF 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 VANLTVVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 SFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLER---EFWLGNDKIHLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 greisaledcaqeqmrlraqvrlletrvk-----qqqvkikqllqenevq-fldkg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 KSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     52;
Hepatic parenchymal cell growth promoter peptide · is isolated from human or animal liver cell or produced by recombinant techniques and used for therapy of liver diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
                                                                                                                                                                                                                                                                                                                                                                                            Length 312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor tyrosine kinase; AR-1; angiogenesis regulator; neoplastic disease; tumour angiogenesis; wound healing; thromboembolic disease; atherosclerosis; inflammatory d
                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                            Score 521; DB 15;
Pred. No. 3.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400 WGTWPGINQAQPGGYKSSFKQAKMMIRPKNFKP
                                                                                                            Claim 2; Page 34; 47pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä.
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ID Y23736 standard; Protein; 346
                                                                                                                                                                                                                                                                                                                                                                                            22.3%;
37.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                               AA;
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Gurney AL;

tumors

98WO-US19093. 97us-0960507

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This sequence is the human tyrosine kinase containing Ig and EGF homology domains (TIE) ligand of the invention, designated NL4. The TIE receptors are receptor tyrosine kinases which are expressed in vascular endothelial cells and early haemopoietic cells. The TIE receptors are believed to be actively involved in angiogenesis, and may play a role in haemopoiesis as well. The TIE ligand homologs can promote the survival and/or growth and/or differentiation of TIE receptor expressing cells. They can be used for promoting neovascularisation in wound healing and for promoting angiogenic processes, such as for inducing collateral vascularisation in a ischemic heart or limb, or for promoting bone development and/or maturation and/or growth in a patient or muscle growth and development. The TIE ligand homologs and antibodies can inhibit the growth of endothelial cells and induce apoptosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated TIE ligand homologs for, e.g. developing products for
                                                                                                                                                                                                                                                                                                         Botstein D, Ferrara N, Goddard A, Godowski PJ,
Hillan K, Roy M, Schwall R, Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 14; 132pp; English.
                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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     WO9915653-A2
                                                                                                              14-SEP-1998;
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                                                                                                                                                                                                                                                                    AR-1, which is related to TIE ligands. AR-1 is believed to be a regulator of angiogenesis and thus the factor, as well as nucleic acids encoding it, are useful in the diagnosis and treatment of certain diseases such as neoplastic diseases involving tumour angiogenesis, wound healing, thromboembolic diseases, atherosclerosis and inflammatory diseases. AR-1 can also be used to support the survival and/or growth and/or migration and/or differentiation of human AR-1 receptor expressing cells. AR-1 can be used to identify the AR-1 receptor. AR-1-cytotoxic conjugates can be used to target tumours expressing AR-1 or its receptor. Its biological activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 NIENYVDNKVANLTVVVNSLDGKCSKCPSQEHMQSQPVQHL-----IYKDCSDHYVLG 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 346;
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                                                                                                                                                                                                                       Example 4; Fig 4A-B; 50pp; English.
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                                                                                                        N-PSDB; X85783
                            Valenzuela DM;
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14;
cells, particularly tumour cells. They can inhibit vasculogenesis, particularly the vascularisation of tumour cells. The antibodies can also inhibit vascularisation of a cell in which a gene encoding an NLI, NLS, NLB or NL4 polypeptide is amplified. The products can also be used for detection, diagnosis, drug screening and production of transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                   104 HRDPGGNGGNGAETAEDSRVQELESQVNKLSSELK - NAKDQIQGLQGRLETLHL - VNMN 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 NIENYVDNKVANLTVVVVNSLDGKCSKCPSQEHMQSQPVQHL-----IYKDCSDHYVLG
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                                                                                                                                                                                                                                                                                                                                                                        54; Mismatches 121;
                                                                                                                                                                                                                                                                                                               DB 20;
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Search completed: February 27, 2001, 12:48:40 Job time: 65 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description		Q14314 homo sapien	Q9ndq1 ciona intes	077802 bos taurus	Q9p2y7 homo sapien	015123 homo sapien	Q9pu54 qallus qall	Q9nrr7 homo sapien	Q08830 homo sapien	Q9u8w8 tachypleus	043827 homo sapien	O35608 mus musculu	093568 qallus qall	Q15389 homo sapien	095841 homo sapien	Q9uku9 homo sapien	Q9u8w6 tachypleus	O08538 mus musculu	Q9r045 mus musculu	Q9u8w7 tachypleus
SUMMARIES	d.	' i	4 Q14314	5 Q9NDQ1	6 077802	4 Q9P2Y7	4 015123	13 Q9PU54	4 Q9NRR7	4 Q08830	5 Q9U8W8	4 043827	11 035608	13 093568	4 Q15389	4 095841	4 Q9UKU9	5 Q9U8W6	11 008538	11 Q9R045	5 Q9U8W7
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П	014314	01-NOV-1996 01-NOV-1996	UI-JUN-ZUOU (TrEMBLrel. FIBRINOGEN-LIKE PROTEIN	Homo sapiens (Human).	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; NCBI TaxID=9606;	1	SEQUENCE FROM N.A.	IISSUE=SMALL INTESTINE; MEDLINE=95369700: PubMed=7642106:	Ruedq C., Pytela R.;	"Sequence of a human transcript expressed in T-lymphocytes	encoding a fibrinogen-like protein.";	Gene 160:257-262(1995).	2]	SECOENCE FROM N.A.	Yuwaraj S., Liu M., Marsden P., Levy G.;	"Cloning and characterization of Hfgl2: The human counterpart to	mouse gene Fg12.";	Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases	EMBL.	EMBL:	HSSP; P02671; 1FZD.	INTERPRO; IPR002181;	PFAM; PF00147; fibrinogen_C; 1	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN;	SEQUENCE	Query Match	best Local Similarity 77. Matches 341; Conservative
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                                                          ---KCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMET 239
                                                  AE-TAEDSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKVANL 173
                                                                                                                           SEQUENCE FROM N.A.
Hotta K., Takahashi H., Asakura T., Saitoh B., Takatori N., Satou Y.,
Satoh N.;
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MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVS
                          LPTLTIQLPRQLGSMEEVLKEVRTLKEAVDSLKKSCQDCKLQADDHRDPGGNG----GNG
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Cionidae; Ciona.
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TISSUE-ADRENAL CORTEX;

X MEDLINE-98451564; Pubbed=9776732;

Mandriota S.J., Pepper M.S.;

"Regulation of angiopoietin-2 mRNA levels in bovine microvascular:

T endothelial cells by cytokines and hypoxia.";

Circ. Res. 83:852-859(1998).

E PUNCTION: BINDS TO TIEZ PREEPFOR AND COUNTERACTS BLOOD VESSEL

MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1 (ANG-1). ITS

FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC

INDUCERS, SUCH AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX

CONTACTS MAY INDUCE ENDOTHELIAL CELL ADOPTOSIS WITH CONSEQUENT

VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY PACILITATE

ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A

PERMISSIVE ANGIOCENIC SIGNAL.
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                                                                                             396 FTSRILRATNPTPVQDGQTESLPY-DCAELYARGVRQSGVYDIRPGTK-VTWTVYCDMDT 453
                                                                                                                                                                                        LEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTPDRDN 356
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Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
"Analysis of blood vessel maturation processes during cyclic ovarian
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SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                             MGGGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLT---KSKEMILRID
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6F086C4A5C80050A CRC64;
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EMBL; AF094699; AAC62490.1; -.
EMBL; AF032924; AAC78285.1; -.
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01-NOV-1998 (TrEMBLrel. 08
01-OCT-2000 (TrEMBLrel. 15
ANGIOPOLETIN-2 (FRAGMENT).
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334 DALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKG 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               angiogenesis.";
Science 277:55-60(1997).
Science 277:55-60(1997).

-1- FUNCTION: BINDS TO TIEZ RECEPTOR AND COUNTERACTS BLOOD VESSEL MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1 (ANG-1). ITS FONCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH AS VOEGF, ANGZ-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR REGRESSION IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE ANGIOGENIC SIGNAL.
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                                                                           EKKIVTATVNNSVLQKQQHDLMETVNNLLTMMSTSNSKDPTVAKEEQISFRDCAEVFKSG
                                                          214 RRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLER
                                                                                                                        EFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAG
                                                                                                                                                   351 EYWLGNEFVSQLTNQQRYVLKIHLKDWEGNEAYSLYEHFYLSSEELNYRIHLKGLTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Walkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buthele Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606;
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
DGKC----SKCPSQEHMQSQPVQHLI--
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-OCT-2000 (TrEMBLrel. 15,
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Matches 135;
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                                                                                                                                                               74 KVLDMEDKHIVQLRSIKEEKDQLQVLVSKQNSIIEELEKQLVTATVNN-----SVLQKQQ 128
                                                                                                                                                                                                                | : | : | : | : | HDLMETVNNLLTIMSTSNPSYSLLAKDEQIIFRDCGEAFKSGLTTSGVYTLTFPNSTEEI 188
                                                                                                                                                                                                                                                                                                                                                    304
                                                                                                                                                                                                                                                                                                                                                                                352 PDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKGVR-NGIFWGTWPGINQAQ 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----LETLHLVNMNNIENYVD------NKVAN-----LTVVVVNSLDGKCSKCPSQE 191
                                                                                                                                                                                             HMQSQPVQHL -------IYKDCSDHYVLGRRSSGAYRVTPDHRNSSF 231
                                                                                                                                                                                                                                                           EVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEM 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 KLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV------NKL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSELKNAKDQIQGLQGR-----LETLHLVNMNNIENYVDN---KVANLTVVVNSL 180
                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                          83;
              Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Biologic significance of angiopoietin-2 expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Tanaka S., Mori M., Sugimachi K., Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.8%; Score 534; DB 4; Length 495
29.5%; Pred. No. 6.3e-32;
.ive 80; Mismatches 153; Indels
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hepatocellular carcinoma.";
J. Clin. Invest. 103:341-345(1999).
EMBL; AB009865; BAA95590.1; -.
SEQUENCE 495 AA; 56848 MW; EBFAC35ABF1F08F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
           Score 541.5; DB 6;
Pred. No. 1.2e-32;
3; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     495
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                                         53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 -SGY--SLKATTMMIRPADF 375
                                                                                                                                                                                                                                                                                                                                                                                                                                            411 PGGYKSSFKQAKMMIRPKNF 430
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                                         Matches 128; Conservative
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Best Local Similarity
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G.D.; in vivo

Euteleostomi;

16; Gaps CEGSQCPF----QLTLPTLTIQLPRQLGSMEEVLKE----VRTLKEAV-DSLKKSCQDC 97 4; Length 496; 22.8%; Score 533.5; DB 4; 29.4%; Pred. No. 6.9e-32; tive 80; Mismatches 153; 48 ò

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                                                   : | :: : | | | : :|| | ODNAYONQTARLELQLLEHSLSTNKL 170
                                                                                                                                                                                                   | ::| | :| :| | | GHTTNGIYETFPNSTEEIKAYCDMEAGGGGWTIIQRREDGSVDFQRTWKEYKVGFGNPS 350
                                                                                                                                                                                                                                     273 REFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTA 332
                                                                                                                                                                                                                                                               410
                                                                                                                                                                                                                                                                                       GDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYK 392
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                   EKQILDQTSEINKLQDKNSFLEKKVLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEEL
                                                                                                                                                                                                                                                    134 SSELKNAKDQIQGLQGR------LETLHLVNMNNIENYVDN---KVANLTVVVNSL
                                                                                                                                      ----YKDCSDHYVL
                                                                                                                                                            EKKIVTATVNNSVLQKQQHDLMETVNNLLTMMSTSNSAKDPTVAKEEQISFRDCAEVFKS
                                                                                                                                                                                      GRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mezquita J., Mezquita B., Pau M., Mezquita C.;
"Characterization of a novel form of angiopoietin-2 (Ang-2B) and
expression of VEGF and angiopoietin-2 during chicken testicular
development and regression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SEQUENCE 407 AA; 46647 MW; E10C03D07E410013 CRC64;
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Last sequence update)
Last annotation update)
                                    KLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV-----
                                                                                                                                                                                                                                                                                                                                      393 GVR-NGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNF 430
                                                                                                                                                                                                                                                                                                                                                       Query Match 22.7%; Score 532; DB 13;
Best Local Similarity 33.8%; Pred. No. 6.9e-32;
Matches 136; Conservative 62; Mismatches 130;
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EMBL; AJ131923; CAB59200.1; -.
HSSP: PO2671; 1FZD.
INTERPRO; IPR002181; -.
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                                                                                                                                     DGKC----SKCPSQEHMQSQPVQHLI-----
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177 ELEKKIVTATVNNSVLOKQQHDLMETVNNLLTMMSTSNSAKDPTVAKEEQISFRDCAEVF 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 ETAEDSRVQELESQVNK - LSSE - - - - - LKNAKDQIQGLQGRLETLHLVNMNIEN 164
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                                                                                                                                     FKSGLTTSGTYILTFPNSAQEKKAYCDMESNGGGWTVLQRREGGSVDFHRTWKEYKIGFG
                                                                                                                                                                                                     270 NLEREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYN
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"Characterization and expression of a novel alternatively spliced human angiopoletran-1.";
J. Biol. Chem. 275:18556.18556(2000).
EMBL: AF187858; AAF76526.1;
SEQUENCE 444 AA; 50958 MW; E512409CE73987A1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 LEREFWIGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.4%; Score 524.5; DB 4; ilarity 34.6%; Pred. No. 2.8e-31; Conservative 57; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                374 RONNNKFNGIKWYYWKG-----SGY--SLKATTWMIRPADF
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ANLTVVVNSLDGKCSKCPSQEHMQSQPVQHLI
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Mammalia; Eutheria; Primates;
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Best Local Similarity
Matches 118; Conserv
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Q9NRR7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 ILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRH-----YNHD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 VVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 AETAEDSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKVANLT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 CDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLER----EFWLGNDKIHLLTKSKEM 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 LRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKG-VRNGIFWGTWP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                                                                                                      related gene, HFRĒP-1.";
Biochem. Biophys. Res. Commun. 193:681-687(1993).
-!- SUBCELLULAR LOCATION: EXTRACELLULAR (PROBABLE).
-!- TISSUE SPECIFICITY: OVEREXPRESSED IN HEPATOCELLULAR CARCINOMAS.
-!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
EMBL; D14446; BAA03336.1; -.
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF FIBRINGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.2%; Score 519.5; DB 4; Length 33.8%; Pred. No. 4.2e-31; ive 47; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOTENTIAL.
FIBRINGEN-LIKE PROTEIN 1.
BETA/GAMMA CHAINS OF FIBRIN BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 2330F3D60CD0BBA8 CRC64;
                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
FIBRINOGEN-LIKE PROTEIN 1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 AA
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Plasma; Blood coagulation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                          TISSUE-HEPATOMA;
MEDLINE-93290661; PubMed-8390249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 33.89 les 131; Conservative
                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR002181; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296
                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
70
83
248
312 AA;
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                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                Hirohashi S.;
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DISULFID
DISULFID
SEQUENCE
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8
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Matches
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RESULT
Q08830
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61 AQPIVSPDPTDCADILLNGYRSSGGYRIWPKSWMTVGTLNYYCDMETDGGGWTV1QRRGN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 -LDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALY 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYS 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                   Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
                                                                                                                                                                                                                  SEQUENCE FROM N.A.

GORUdan S., Muta T., Tsuda R., Koori K., Kawahara T., Seki N.,
Mizunoe Y., Wai S.N., Iwanaga S., Kawabata S.;
Misunoe ri, Wai S.N., Iwanaga S., Kawabata S.;

Misunoe ria acetyl group-recognizing lectins involved in innate immunity are structurally related to fibrinogen.";

Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).

EMBL; AB024737; BAA84188.1; -.

INTERPRO: IPR002181; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 SQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDH--RNSSFEVYCDMETMGGGWTVLQAR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 292;
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                    PFAN; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SEQUENCE 292 AA; 33786 MW; D028DE1E2716F71A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                          Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 21.9%; Score 513.5; DB 5; Best Local Similarity 42.7%; Pred. No. 1.1e-30; Matches 103; Conservative 38; Mismatches 81;
AA.
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                                       Created)
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              Q9U8W8;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2000 (TrEMBLrel. 15,
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06,
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PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=6853;
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                                                                                                TECHYLECTIN-5A.
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01-JUN-1998 (
01-MAY-2000 (
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RESULT
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                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                        104 HRDPGGNGGNGAETAEDSRVQELESQVNKLSSELK--NAKDQIQGLQGRLETLHL-VNMN 160
                                                                                                                                                                                                                                                                                 214 RRSSGAYRVTPDH--RNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNL 271
                                                                                                                                                                                                                                                                                                                                                                                    272 EREFWIGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGT 331
                                                                                                                                                                                                                                                                                                                                                                                                       258 VGNDALQY ----HNNTAFSTKDKDNDNC-LDKCAQLRKGGYWYNCCTDSNLNGVYYRLG 311
                                                                                                                                                                                                                                                              161 NIENYVDNKVANLTVVVNSLDGKCSKCPSQEHMQSQPVQHL-----IYKDCSDHYVLG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                AG-DALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYY--- 387
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                   MEDINE-97349327; PubMed-9204896; Maisonpierre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J., Radisonpierre P.C., Compton D.L., McClain J., Aldrich T.H., Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.; "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1 (ANG-1). ITS FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: BINDS TO TIEZ RECEPTOR AND COUNTERACTS BLOOD VESSEL
                                                                                                                                                                         48;
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                                                                                                                                      21.7%; Score 507; DB 4; Length 346; 35.5%; Pred. No. 4.1e-30; Live 54; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |: :|| | | | | | | 312 EHNKH---LDGITWYCWHGSTY-----SLKRYEMKIRPEDFKP 34'6
                                          HSSP; P02671; IFZD.
INTERPRO; IPR002181; -.
PFAM; PF00147; fibrinogen_C; 1.
SEQUENCE 346 AA; 40018 MW; AEC0A601CC498B43 CRC64;
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Last annotation update)
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              EMBL; Y16132; CAA76078.1; -. EMBL; AL049653; CAB44734.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                      Best Local Similarity 35.59
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenesis.";
Science 277:55-60(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                         Query Match
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SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF THE BETA AND GAMMA CHAINS OF FIBRINGEN.

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174 TVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 DSRVQELESQVNKLSSELKNAKDQIQGLQGRLETL-----HLVNMNNIENYVDNKVANL 173
                                                                                                                                                                                                                                                                                                                 YCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEMIL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                            RIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTPD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 KIQLKDWEGNEAHSLYDHFYLAGEESNYRIHLTGLTGTAAKISSISQPGSD----FSTKD 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 RDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKGVR-NGIFWGTWPGINQAQPG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                252 METVNSLLTWMSSPNSKSSVAIRKEEQTTFRDCAEIFKSGLTTSGIYTLTFPNSTEEIKA
                                                                                                                                                                                                                             21.6%; Score 506; DB 11; Length 496; 35.2%; pred. No. 7.6e-30; tive 55; Mismatches 131; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cao Y., Waissbach L., Fu Y., Grieninger G.;
"Chicken fibrinogen gamma chain mRNA.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF087432; AAC36476.1;
HSSP, P02679; 2FTB.
INTERPRO, IPR002181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
FIBRINGEN GAMMA CHAIN.
91D2BC7FE86E0766 CRC64;
                                                                                                                                                                           FA3021FE4E01C410 CRC64;
                                                                                                                                  (POTENTIAL).
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Last annotation update)
                                                                                                                                  COILED COIL (POTENTIAL FIBRINOGEN BETA/GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                               PFAM; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN;
                                                                                                                                                                 POLY-GLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBRINGEN GAMMA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49642 MW;
                                                                                                                                                                321 P
56616 MW;
EMBL; AF004326; AAB63189.1;
HSSP; P02671; 1FZD.
MGD; MGI:1202890; Agpt2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 GY--SLKATTMMIRPADF 496
                                                                                                                                                                                                                                                               Conservative
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01-NOV-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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                                                   INTERPRO; IPR002181;
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435 AA;
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159
282
318
496 AA;
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nes 112; Conserv
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                                                                                                  Coiled coil
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SEQUENCE
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Matches
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PGGYKSSFKQAKMMIRPKNF 430
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CARBOHYD
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SEQUENCE
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                                             17;
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                                                                                                                                                                                        -----YPSEKQTLPQSIEQLTQKSKKIIEEII----RY 122
                                                                                                                                                                                                                                                                         265
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                                                                                                                                                                                                                                                                                                                                                                                                            266 AGFGNLE----REFWLGNDKIHLLTKSKEM--ILRIDLEDFNGLTLYALYDQFYVANEFL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 KSCQDCKLQADDHRDPGGNGGNGAETAEDSRVQELESQVNKLSSELKNAKDQIQGLQGRL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 KYRLTYAYFIGGERGDAFDGFNFGDDPSDKSYTYHNGMR-FSTFDNDNDNF-EGNCAEQD 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 SSGWWFDSCLSANLNGKYY ---- HQKYKGVR---NGIFWGTWPGINQAQPGGYKSSFKQA 421
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Momura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y., Sato S., Nagase T., Seki N., Ishikawa K.I., Tabata S.; "Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid
                                                                                     91
                                                                                                                          93
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                                                                                                                                                                                                                                                                                                                                                                                                                                   239 EGFGHLSPDDFTEFWLGNEKIHLITTQSTLPYALRIELEDWSGKKGTADYAVFKVGTEED
                                                                                                                                                                                                                                                152 ETLHLVNMNNIENYVD-----NKVANLTVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKD
                                                                                     ------FOLT-----LPTLTIQLPRQLGSMEEVLKEVRTLKEAVDSLK
                                                                                                           42 GSYCPTTCGIADFFNKYRLTTDGELLEIEGLLQQATNSTGSIEYLLQHIKTI-----
                                                                                                                                                                                                                                                                                                                               CSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KYRL----HIGNYNGTAGDALRF----SRHYNHDLRFFTTPDRDNDRYPSGNCGLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                             101;
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MEDLINE-97134663; PubMed-8980223;
Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L.,
Ryan T.E., Bruno J., Radziejewski C., Malsonpierre P.C.,
      Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a ligand for the TIE2 receptor,
                                             140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
      DB 13;
Score 489.5; DB 1
Pred. No. 1.1e-28;
1; Mismatches 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 307-498 FROM N.A. MEDLINE-96051387; PubMed=7584026;
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MEDLINE=96051389; PubMed=7584028;
                                           51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yancopoulos G.D.;
"Isolation of angiopoietin-1,
    20.9%;
31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01,
05,
15,
                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANGIOPOIETIN-1 (ANG-1).
ANGPT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1:27-35(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                        Similarity
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01-JAN-1998
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      Query Match
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Q15389;
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IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR
PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
                                                                                                                                                                                                                                              TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL PROCESSES LATER AND DISTINGRY FROM THAT OF VEGF. APPEARS TO PLAY A CRUCIAL ROLE IN MEDIATINGRY FROM THAT OF YEAR. BETWEEN THE ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
                                                                                                                                                                                                                                                                                                                                                                      VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE HEART EARLY DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AVQNHTATMLEIGTSLLSQTAEQTRKLTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 GSMEEVLK--EVRTL------KEAVDSLKKSCQDCKLQADDHRDPGGNGGNGAE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351
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Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y., Sato S., Nagase T., Seki N., Ishikawa K.I., Tabata S.; "Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)."; DNA Res. 1:47-56(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISCHEMIC HEART.
-!- SIMITARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART THE BETA AND GAMMA CHAINS OF FIBRINGEN.
-!- PTM: GLYCOSYLATED.
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N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
SD5FA63AEF6BE920 CRC64;
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31.1%; Pred. No. 1.4e-2...
...e 70; Mismatches 145; ...ncsOCPF
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Glycoprotein; Coiled coil.
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Matches 137;
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Search completed: February 27, 2001, 12:49:37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 PPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLMCENSLDPGGWTVIQKRTD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKEAVDSLKKSCQDCKLQADDHRDPGGNGGNGAETAEDSRVQELESQVNKLSSELKNAKD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---QIQGLQGRL--ETLHLVNMNNIENYVDNKVANLTVVVNS-----LDGKCSKCPSQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ODTHVSPPLVQVVPQHIPNSQQYTPGLLGGNEIQRDPGYPRDLMPPPDLATSPTKSPFKI 266
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                                                                                                                                                                                                                                                                                                                                                                                                                               42 GKEEAKKCAYTFLVPEQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREIDV 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLD
                                                                                                                      ANGIOPOIETIN Y1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                             Query Match 20.9%; Score 488; DB 4; Length 491; Best Local Similarity 27.0%; Pred. No. 1.6e-28; Matches 129; Conservative 80; Mismatches 143; Indels 126;
                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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-----SLRSTTMMIRPLDF 498
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EMBL, AF107253; AAD19608.1;
HSSP; P02671; 1F2D.
                                                                                       01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-2000 (TrEMBLrel. 13,
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                                                                  PRELIMINARY;
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                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=9606;
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Q9UKU9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 IQLPRQLGSME-EVLKEVRTLKEAVDSLKKSCQDCKLQADDHRDPGGNGGNGAETAEDSR 122
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                                                                                                                                                                                                                                                                              TISSUE-HEART;
MEDLINE-99403103; PubMed=10473614;
Kim I., Moon S.O., Koh K.N., Kim H., Uhm C.S., Kwak H.J., Kim N.G.,
Koh G.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 W-WL--GLLAAMGAVAGGEDGFEGTEEGSPREFIYLNRYKRAGESO-DKCTYTFIVPQQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 VQELESQVNKLSSELKNAKDQIQGLQGRLETLHL-------VNMNNIENYVDNK
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                                                                                                                                            Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SEQUENCE 493 AA; 57104 MW; 0F2ADECE53D185CA CRC64;
                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.7%; Score 483.5; DB 4;
Best Local Similarity 26.3%; Pred. No. 3.6e-28;
Matches 136; Conservative 84; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 SR-YQDGVYWAEFRG-----GSY--SLKKVVWMIRP 487
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EMBL: AF125175; AAD55357.1; -.
HSSP: P05671; 1FZD.
INTERREN: IPRO02181; -.
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2000 (TrEMBLrel. 15, Last ann
                                                                                   ANGIOPOIETIN-RELATED PROTEIN-2.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=9606;
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; MOLECULE TYPE: protein US-08-525-505A-2
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                                                                                                                                                                              February 27, 2001, 12:48:04; Search time 21.07 Seconds
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-373-579-6
US-08-18-555-56
US-08-665-926-6
US-08-65-926-6
US-08-960-507-19
US-08-960-507-19
US-08-37-579-4
US-08-18-595-4
US-08-18-595-4
US-08-18-595-4
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US-08-206-176-6
US-08-933-821-2
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Listing first 45 summaries

    protein search, using sw mode.

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        19.9
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        US-08-434-099A-28
        Sequence 28, Appl 30
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        US-08-812-586-49
        Sequence 4, Appl 31
        Appl 32
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        Appl 33
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        3
        US-08-912-16
        Sequence 6, Appl 33
        Appl 33
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        Sequence 6, Appl 34
        Appl 34
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        US-08-404-651-4
        Sequence 4, Appl 36
        Appl 36
        Appl 36
        Appl 36
        Appl 37
        Appl
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ALIGNMENTS

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US-08-525-505A-2

Sequence 2, Application US/08525505A

Patent No. 5807711

GENERAL INFORMATION:

APPLICANT: HARA, HIROSHI
APPLICANT: HARA, HIROSHI
APPLICANT: HARA, HIROSHI
APPLICANT: SHINDO, SAEKO
APPLICANT: HARADA, KAZUNORI
ITILE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
NUMBER OF SEQUENCES: 7
CORRESSED OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: 09LON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: 010N, SPIVAK, MCCLELLAND, WAIER & NEUSTADT,
ADDRESSEE: 05. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
COUNTY: USA
IP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: DAY
CORREY: DAY
CORREY: DAY
CORREY APPLICATION DAYA:
APPLICATION NUMBER: US/08/525,505A
FILING DATE: 22-MR-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REDRICKER CHARACTERISTICS:
LENGTH: 314 amino acids
TTPE: MUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBE
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411 GKISSISQPGND----FSTKDGDNDKCIC-KCSQMLTGGWWFDACGPSNLNGMYPQRQN 465
                                                                                                                                                                                                                                                                                                                                                                                                                                             98 KLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV---------NKL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 SSELKNAKDQIQGLQGR-----LETLHLVNMNNIENYVDN---KVANLTVVVNSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 GRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 REFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 GDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYK 392
                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 DGKC-----SKCPSQEHMQSQPVQHLI------YKDCSDHYVL
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TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
TITLE OF INVENTION: THEREOF
WUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   Length 496;
                                                                                                                                                                                                                                                                                                                                               Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             22.8%; Score 533.5; DB 1; 29.4%; Pred. No. 3.7e-43; tive 80; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 GVR-NGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNF 430
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FILING DATE: 06-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08418595
Patent No. 5814464
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               Matches 135; Conservative
      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                                                                                                                                                      , MOLECULE TYPE: protein US-08-373-579-6
                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                       amino acid
                                                                                                                                   linear
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                                                                                              TYPE: amir
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 RFFTTPDRNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKG-VRNGIFWGTWPG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 EDSRVQE---LESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKVANLTV 175
                                                                                                                                                                                                                                                 176 VVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYC 235
                                                                                                                                                                                                                                                                                                                                                                     DMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLER---EFWLGNDKIHLLTKSKEMI 292
                                                                        Gaps
                                                                                                                                                                                        75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 DENCLOEQVRLRAQVROLETRVKQQQVVIAQLLHEKE-VQFLDRGQEDSFID-----
                                                                 53;
   Length 314;
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Patent No. 5650490
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
; Score 533.5; DB 1; Length 3:
; Pred. No. 1.8e-43;
46; Mismatches 103; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,579
FLING DATE: 17-JAN-1995
PRIOR APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 77 Old Saw Mill River Road CITY: Tarrytown STATE: New York COUNTRY: USA
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REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/330,261 FILING DATE: 27-0CT-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/319,932 FILING DATE: 07-0CT-1994 ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 INQAQPGGYKSSFKQAKMMIRPKNFKP 432
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   22.8%;
38.2%;
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                                                              Matches 125; Conservative
                                  Similarity
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TELEFAX: (
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   Query Match
Best Local
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926 FILING DATE: 19-JUN-1996 CLASSIFICATION: 435
                                                                ADDRESSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICALLOR

FILING DATE: 19-JUN-1>>
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
REGISTRATION NUMBER: REG 330-H
TELECOMMUNICATION INFORMATION:
"WITEPHONE: (914) 345-7400
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (914) 345-2113
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHRRACTERISTICS: LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 29.44
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-665-926-6
   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
                                                                                                                          Tarrytown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYK 392
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Patent No. 5851797
GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.8%; Score 533.5; DB 2; 29.4%; Pred. No. 3.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466 TNKFNGIKWYWKG-----SGY--SLKATTMMIRPADF 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 KLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGKC----SKCPSQEHMQSQPVQHLI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: REG 330-D TELECOMMUNICATION INFORMATION:
17-JAN-1995
JMBER: US 08/353,503
09-DEC-1994
                                                                            PRILIMS DATE: 0. 2.2.7.7.

APPLICATION DATA: APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
APPLICATION DATA: US 08/330,261
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            36,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-721
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cobert, Robert J
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 29.4
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-418-595-6
   FILING DATE: 17-JAN APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                          NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 EKKIVTATVNNSVLQKQQHDLMETVNNLLTMMSTSNSAKDPTVAKEEQISFRDCAEVFKS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 KLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV---------NKL 133
                                                   Gaps
                                                                                                 48 CEGSQCPF----QLTLPTLTIQLPRQLGSMEEVLKE----VRTLKEAV-DSLKKSCQDC 97
                                                                                                                                                                                                                                                                                                                                                   171 EKQILDQTSEINKLQDKNSFLEKKVLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 GDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTA
                                              91;
Length 496;
                                                Indels
22.8%; Score 533.5; DB 2; 29.4%; Pred. No. 3.7e-43; Live 80; Mismatches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 GVR-NGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNF 430
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US-09-162-437-6
; Sequence 6, Application US/09162437
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291 GHTINGIYILIFPNSIEEIKAYCDMEAGGGGWTIIQRREDGSVDFQRTWKEYKVGFGNPS 350
                                                                                                                                                                                                                333 GDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYK 392
                                                                                                                                                                                                                                         231 EKKIVTATVNNSVLQKQQHDLMETVNNLLTMMSTSNSAKDPTVAKEEQISFRDCAEVFKS 290
                                          213 GRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE 272
                                                                                                                            273 REFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTA 332
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APPLICANT: HARA, HIROSHI
APPLICANT: YOSHIMURA, HIROMITSU
APPLICANT: MATSUKI, YUMIKO
APPLICANT: SHINDO, SAEKO
APPLICANT: HANADA, KAZUNORI
TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.4%; Score 524; DB 1; Length 312; 37.8%; Pred. No. 1.5e-42; Live 41; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CHIY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,505A
                                                                                                                                                                                                                                                                                                   393 GVR-NGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNF 430
                                                                                                                                                                                                                                                                                                                                           466 TNKFNGIKWYYWKG-----SGY--SLKATTMMIRPADF 496
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00455
FILING DATE: 22-MAR-1994
APPLICATION NUMBER: J905-063905
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08525505A Patent No. 5807711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 45F
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: 703-413-2220
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Best Local Similarity 37.85
Matches 126; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-525-505A-4
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US-08-525-505A-4
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171 EKQILDQTSEINKLQDKNSFLEKKVLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 496;
                                                       TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLQADDHR-----DPGGNGGNGAETAEDSR-VQELESQV---
                                                                                                                                         ADDRESSEE: Regeneron Pharmaceuticals, Inc. STREET: 77 old Saw Mill River Road CITY: Tarrytown STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-3NN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,43
                                                                                                                                                                                                                                                                                              S: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/418,595
FILING DATE: 06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 496 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                     Davis, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-09-162-437-6
                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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           GENERAL INFORMATION:
APPLICANT: Davis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                              COUNTRY: US
ZIP: 10591
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                               SOFTWARE
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307 ALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGL 366 :||: ||: || ||: || ||: || ||: ||
                             | : ::||:: :|||: | 11|| | 11||: | 55 SNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLFFPNSTEEIKAYCDMEAGGGGWTI 114
                                                                                                                                                                                                                                                                                            LQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLY 306
                                                                                                                                                                                                                        175 SLYEHFYLSSEELNYRIHLKGLTGTAGKISSISQPGND----FSTKDGDNDKCIC-KCSQ 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 HRDPGGNGGNGAETAEDSRVQELESQVNKLSSELK--NAKDQIQGLQGRLETLHL-VNMN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 HKTPAQPQLKAANCCEE--VKELKAQVANLSSLLSELNKKQERDWVSVVMQVMELESNSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 NIENYVDNKVANLTVVVVNSLDGKCSKCPSQEHMQSQPVQHL-----IYKDCSDHYVLG
  CPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTV
                                                                                                                                                                                                                                                                   367 YYSSGWWFDSCLSANLNGKYYHQKYKGVR-NGIFWGTWPGINQAQPGGYKSSFKQAKMMI
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Best Local Similarity 35.5%; Pred. No. 7.5e-41;
Matches 123; Conservative 54; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/08960507 Patent No. 6057435 GENERAL INFORMATION:
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ATORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REPRENCE/POCKET NUMBER: P113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 19:
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282 RPADF 286
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                                                                                                                   67 DENTVVDLGS------KRQ------YADCSEIFNDGYKLSGFYKIKPLQSPA 106
                                                                                                                                                                                                  107 EFSYYCDMSD-GGGWTVIQRRSDGSENFNRGWRDYENGFGNFYQKHGEYWLGNKNLHFLT 165
                                                                                                                                                                                                                                                                                          .70 VANLIVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNS 229
                                                                                                                                                                                                                                                                                                                                                       342 -YNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQKYKG-VRNGIF 399
112 GNGAETAEDSRVQE--LESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNK 169
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                                        17 GREISALEDCAQEQMRLRAQVRLLETRVK------QQQVKIKQLLQENEVQ-FLDKG 66
                                                                                                                                                                           230 SFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLER---EFWLGNDKIHLLT
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          400 WGTWPGINQAQPGGYKSSFKQAKMMIRPKNFKP 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 WYTW-----HGWWYSLKSVVMKIRPNDFIP 309
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NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130p1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 560/225-3216
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/08960507
Patent No. 6057435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: GUTNEY, AUSTIN L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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CITY: South San Francisco
STATE: California
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Amino Acid
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Matches 110; Conservative
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Mismatches 145;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17.-AN-1995
APPLICATION NUMBER: US 08/353,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MBER: US 08/348,492
02-DEC-1994
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09-DEC-1994
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FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 GGYKSSFKQAKMMIRPKNF 430
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----SLRSTIMMIRPLDF 497
 Conservative
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COMPUTER READABLE FORM:
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Matches 137;
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                                    258 VGNDALQY-----HNNTAFSTKDKDNDNC-LDKCAQLRKGGYWYNCCTDSNLNGYYRLG 311
                                                                                    272 EREFWLGNDKIHLLTKSKEMILRIDLEDFNGLFLYALYDQFYVANEFLKYRLHIGNYNGT 331
                                                                                                                                                              332 AG-DALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYY--- 387
             214 RRSSGAYRVTPDH--RNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNL 271
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08373579
Patent No. 5650490
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          388 -HQKYKGVRNGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNFKP 432
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PPLICATION NUMBER: US/08/373,579
FILING DATE: 17-JAN-1995
CLASSIFICATION: 435
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Pred. No. 6.6e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Regeneron Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 777 Old Saw Mill River Road CITY: Tarrytown STATE: New York COUNTRY: USA
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PRIOR PAPLICATION NUMBER: US 08/348,492
PRIOR PAPLICATION DATE:
APPLICATION NUMBER: US 08/330,261
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-0CT-1994
APPLICATION NUMBER: US 08/319,932
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
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31.2%;
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MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                                                                                                 -----KEAVDSLKKSCQDCKLQADDHRDPGGNGGNGAE 116
                                                                                                                                                                                                                                             117 TAEDSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLH-LVNMNNIENYVDNKVANLTV 175
                                                                                                                                                                                                                                                                                                                                              176 VVNSLDGKCSK---CPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFE 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87; Gaps
                                             19 AVEEHNL-----TEGLEDASAQAACPARLEGSGRCEGSQCPFQLTLPTL-TIQLPRQ-L 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08418595
Patent No. 5814464
GENERAL INFORMATION:
APPLICAMT: Davis, et al.
TITLE OF INVENTION: THE-2 LICAND, METHOD OF MAKING AND USES
TITLE OF INVENTION: THEREOF
  Indels
                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: US/08/418,595
FILING DATE: 06-APR-1995
                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
CONWINY: USA
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Best Local Similarity 31.28
Matches 137; Conservative
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New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 DRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQ-KYKGVRNGIFWGTWPGINQAQP 411.
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                                                                                                                                                                                                                                                                                                                                                                                                                           119 AVQNHTATMLEIGTSLLSQTAEQTRKLTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 GSMEEVLK--EVRTL------KEAVDSLKKSCQDCKLQADDHRDPGGNGGNGAE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 ------CTKEVLLKGGKREEDKP-----FRDCADVYQAGFNKSGIYTIYINNMPEPKK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 VYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEMI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 LRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTP 352
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                                                                                                                                                                                                                                                                                                                                                        87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08665926
Patent No. 5851797
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                20.9%; Score 489.5; DB 2; Length 31.2%; Pred. No. 6.6e-39; ive 70; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...urESSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill River Road CITY: Tarrytown STATE: New Vary
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: CODERT, ROBERT J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELEPHONE: (914) 345-7400
TELEPRAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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484 ----SLRSTTMMIRPLDF 497
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 31.2%
Matches 137; Conservative
                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-418-595-4
                                                                                                                                                                                                                        TOPOLOGY: linear
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265 ------CTKEVLLKGGKREEDKP-----FRDCADVYQAGFNKSGIYTIYINNMPEPKK 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 497;
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Sequence 4, Application US/08348492

Patent No. 5879672

GENERAL INFORMATION:

APPLICANT: Davis, et al.

TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES

TITLE OF INVENTION: THEREOF
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 19-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RODERT INFORMATION:

REGISTRATION NUMBER: 36,108

REFERENCE/DOCKET NUMBER: 36,108

REFERENCE/DOCKET NUMBER: 36,108

TELEPANTION INFORMATION:

TELEPANTION INFORMATION:

TELEPANTION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 497 amino acids

TELEPANTION CONTROL OF A 
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31.2%; Pred. No. 6.6e-39;
Live 70; Mismatches 145;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
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COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 TAEDSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLH-LVNMNNIENYVDNKVANLTV 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQ-KYKGVRNGIFWGTWPGINQAQP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 87; Gaps
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                                             COMPUTER TO STATE TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 489.5; DB 2;
; Pred. No. 6.6e-39;
70; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 330B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 347-7000
TELEPHONE: (914) 347-7113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.9%;
Best Local Similarity 31.2%;
Matches 137; Conservative 70
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----SLRSTTMMIRPLDF 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-348-492-4
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COUNTRY:
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119 AVQNHTATMLEIGTSLLSQTAEQTRKLTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 497;
Patent No. 6166185
GENERAL INFORMATION:
APPLICANT: Davis, et al.
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytonk
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.9%; Score 489.5; DB 3; Best Local Similarity 31.2%; Pred. No. 6.6e-39; Matches 137; Conservative 70; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/418,595
FILING DATE: 06-APR-1995
PRIOR APPLICATION NUMBER: US 08/373,579
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-AN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
PRIOR APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT: UNDERFILED
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,437 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REC
                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 497 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                    USA
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US-09:162-437-4 ; Sequence 4, Application US/09162437 Φ

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225 DHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE----REFWLGND 280
                                                                                                                                                                                  KIHLLTKSKEM--ILRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNY-NGTAGDAL- 336
                                                                                                                                                                                                       -----RFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKY 386
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 --- EIYNSNN--- 144
                                                                                                                                                                                                                                                                                           318 GFDFGDDPSDKF--FTSHNGMQFSTWDNDNDKF-EGNCAEQDGSGWWMNKCHAGHLNGVY 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 GKEEAKKCAYTFLVPEQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREIDV 101
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                                     165 YVDNKVANLTVVVNSLDGKCSKCPSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80; Mismatches 143; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                   ----KTRWYSMKKTTMKIIPFN 416
                                                                                                                                                                                                                                                                                                                           387 YH-----QKYKGVRNGIFWGTWPGINQAQPGGYKS---SFKQAKMMIRPKN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 491;
 101 KP----NMIDAATLKSRI--MLEEIMKYEASILTHDSSIRYLQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 2;
9.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94400
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 488;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/933,821
                                                                                                                                                                                                                                                                                                                                                                   375 YQGGTYSKASTPNGYDNGIIWATW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08933821
Patent No. 5972338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 GRCEGSQCPFQLTLPTLTIQLP --
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27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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650/952-9881
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Amino Acid
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SOFTWARE: WinPati
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Best Local Similarity
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CLASSIFICATION:
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TELEFAX: 6
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US-08-933-821-4
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                                                                                                                               -----CTKEVLLKGGKREEDKP----FRDCADVYQAGFNKSGIYTIYINNMPEPKK 311
                                   233 VYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEMI 292
                                                      LRIDLEDFNGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTP 352
                                                                                                                                                                                  353 DRDNDRYPSGNCGLYYSSGWWFDSCLSANLNGKYYHQ-KYKGVRNGIFWGTWPGINQAQP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 GSQCPFQL----TLPTLTIQLPRQLGSMEEVLKEVRTLKEAVDSLKKSCQDCKLQADDHR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 DPGGNGGNGAETAE-DSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIEN 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dalrymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
CORRESPONDENCE 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/206,176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.9%; Score 488.5; DB 1; 32.9%; Pred. No. 7.1e-39; iive 54; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELEPHONE: 206-547-8080 ext 322
TELEPHONE: 206-548-2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: ZymoGenetics, Inc.
4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08206176
Patent No. 5639940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                      412 GGYKSSFKQAKMMIRPKNF 430
                                                                                                                                                                                                                                                                              | : ||||| :|
----SLRSTIMMIRPLDF 497
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 32.9%
Matches 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Garner, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-206-176-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Garner
APPLICANT: Dalrym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seattle
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                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-206-176-6
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STATE:
265
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146	190	206	201	266	252	326	312	386	372	440	7:	6	
102 LQLVVDVDGNIVNEVKLLRKESRNMNSRVTQLYMQLLHEIIRKRD 146	143OIQGLQGRLETLHLVNMNNIENYVDNKVANLTVVVNSLDGKCSKCPSQ 190	147 NSLELSQLENKILLNYTTEMLKMATRYRELEVKYASLTDLVNNQSVMITLLEEQCLRIFSR	191 EHMQSQPVQHL	207 QDTHVSPPLVQVVPQHIPNSQQYTPGLLGGNEIQRDPGYPRDLMPPPDLATSPTKSPFKI	IYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLD	267 PPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDPGGWTVIQKRTD 326		327 GSVNFFRNWENYKKGFGNIDGEYWLGLENIYMLSNODNYKLLIELEDWSDKKVYAEYSSF	313 YVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDLRFFTTPDRDNDRYPSGNCGLYYSSGW 372	RLEPESEFYRLRIGTYQGNAGDSMMWHNGKQFTTLDRDKDMY-AGNCAHFHKGGW 440	WFDSCLSANLNGKYYHQKYKGVRNGIFWGTWPGINQAQPGGYKSSFKQAKMMIRP 427	WYNACAHSNINGVWYRGGHYRSKH-QDGIFWAEYRGGSYSLRAVQMMIKP 489	
102	143	147	191	207	202	267	253	327	313	387	373	441	
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Search completed: February 27, 2001, 12:48:06 Job time: 32 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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February 27, 2001, 12:47:35; Search time 53.35 Seconds (without alignments) 964.466 Million cell updates/sec Run on:

US-09-442-143-2 2378 1 MKLANWYWLSSAVLATYGFL......GYKSSFKEAKMMIRPKHFKP 439 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

374700 segs, 117207915 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% . Listing first 45 summaries

Database :

sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_rodent:*
sp_vrus:*
sp_vrus:*
sp_vertebrate:*
sp_unclassified:* SPTREMBL_15:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_human:*
6: sp_mammal:*
7: sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery Ouery Duery																							
Score Match Length DB ID 2378 100.0 618.5 26.0 652 5 0914 523.5 22.1 375 6 077 523.5 22.0 495 4 0915 520 22.0 496 4 095 520 22.0 496 4 095 520 22.0 496 4 095 520 22.0 496 4 095 520 22.0 496 4 095 520 22.0 496 4 095 505 21.2 491 4 098 485.5 20.4 493 11 099 485.5 20.4 493 11 099 487.5 20.3 488 13 099 486.5 20.3 488 13 099 486.5 20.3 488 11 099 486.5 20.3 488 11 099 486.5 20.3 488 11 099 486.5 20.3 488 11 099 486.5 20.3 488 11 099 486.5 20.3 488 11 099				Description	O14314 homo sapien	Ogndq1 ciona intes	O35608 mus musculu	077.802 bos taurus	Q9p2y7 homo sapien	Q9pu54 qallus qall	015123 homo sapien	Q9nrr7 homo sapien	Q08830 homo sapien	O95841 homo sapien	043827 homo sapien	Q15389 homo sapien	Q9u8w8 tachypleus	Q9r045 mus musculu	O08538 mus musculu	091589 xenopus lae	Q9jj03 rattus norv	Q9uku9 homo sapien	Q9u8w6 tachypleus
Score Match Length DB 2378 100.0 652 5 652 5 652 5 652 5 652 6 652 5 652 6 652	SUMMARIES			۵	14314	9NDQ1	035608	77802	9P2Y7	29PU54	15123	9NRR7	08830	95841	43827	15389	9U8W8	29R045	008538	291589	29JJ03	90109	9U8W6
SCORF 23.78 618.5 524.25 524.25 523.3 523.3 523.3 523.3 523.3 523.3 5489 5489 5489 5489 550 560 570 570 570 570 570 570 570 57					4	2	11	9	4	13	4	4	4	4	4	4	2	11	11	13	11	4	2
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		фP	Query	Match	100.0	26.0	22.1	22.1	22.0	22.0	22.0	21.9	21.3	21.2	20.6	20.5	20.4	20.4	20.3	20.3	20.2	20.2	20.0
Result No. 10. 12. 2. 3. 3. 4. 4. 4. 4. 10. 11. 11. 11. 11. 11. 11. 11. 11. 11				Score	2378	618.5	525	524.5	523.5	523	522	520	506.5	505	489	486.5	485.5	485.5	483.5	482.5	481.5	480.5	476
			Result	No.	1	2	e	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

093568 gallus gall 0948W7 tachypleus 094W46 mus musculu 018920 bos taurus 070165 mus musculu 099264 homo sapien 099428 tagratus norv 028763 papio hamad 029041 sus scrofa 029041 sus scrofa 029041 sus scrofa 0296596 homo sapien 000602 homo sapien 000602 homo sapien 0006131 homo sapien 000531 homo sapien 020531 homo sapien 025752 homo sapien	SO .
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20.0 119.8 119.6 119.0 118.3 118.3 117.7 117.8 117.7 117.7	17.7 17.6 17.6 17.4 17.3 17.0 17.0
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ALIGNMENTS

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549 AGDALNYGENYNHHLQPFTTFDRDNDGYALGNCGRYYRSGWWFNACFAANLNGNYYTGPY 608
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                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Best Local Similarity 32.94
Matches 127; Conservative
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01-JAN-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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256
496
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159 . 2
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496 AA;
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Hotta K., Takahashi H., Asakura T., Saitoh B., Takatori N., Satou Y.,
Satoh N.;
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                                                          61 LPPLTIQLPRQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                  APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL 180
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                                      LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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43.0%; Pred. No. 3.7e-33;
ive 53; Mismatches 91;
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Best Local Similarity 43.0%;
Matches 120; Conservative
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Cionidae; Ciona.
NCBI_TaxID=7719;
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244 LQKQQHDLMETVNSLLTMMSSPNSKSSVAIRKEEQTTFRDCAEIFKSGLTTSGIYTLTFP 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97349327; PubMed-9204896; Maisonpierre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J., Radziejewski C., Compton D.L., McClain J., Aldrich T.H., Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.; Angiopoietin 2, a natural antagonist for Tie2 that disrupts in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i - FUNCTION: BINDS TO TIEZ RECEPTOR AND COUNTERACTS BLOOD VESSEL MATURATION/STABILITY MEDIATED BY ANGIODICTIN-1 (ANG-1). ITS FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH AS VEGF, ANG2-WEDIATED LOOSENING OF CELL-MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 VDSKVANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murinae; Mus.
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-!- TISSUE SPECIFICITY: EXPRESSED ONLY AT SITES OF VASCULAR REMODELING.
-!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART (THE BETA AND GAMMA CHAINS OF FIBRINGGEN.
EMBL; AF004326; AAB63189-1; -. BRISP; POSCA1; 17EZD.
MGD; MGI:1202890; AGPt2.
INTERPRO; IPRO02181; -.
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FA3021FE4E01C410 CRC64;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                           646
RGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                             :||:|||:|||| :||:|
KGVQNGIYWGTWYKLSDS-TSNSRYSFKYYDMKVRPLNF
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Matches 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1 (ANG-1). ITS FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH AS VEGF, ANGZ-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL CELL MAPOPTOSIS WITH CONSEQUENT VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE DEPENDSLYE ANGIOGENIC SIGNAL.

DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN YECKESSION OF CAPILLARIES THAT HAD DEVELOPED PERICYTE CONTACT IN THE MIDSTAGE CORPUS LUTEON.
304 NSTEEIKAYCDMDVGGGGWTVIQHREDGSVDFQRTWKEYKEGFGNPLGEYWLGNEFVSQL 363
                                        TKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=99054348; PubMed=9840613;
Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
"Analysis of blood vessel maturation processes during cyclic ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                     Mandriota S.J., Pepper M.S.;
"Regulation of angiopoietin-2 mRNA levels in bovine microvascular
endothelial cells by cytokines and hypoxia.";
Circ. Res. 83:852-859(1998).
-1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
                                                                                          353 LKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S -> L (IN REF. 2).
6F086C4A5C80050A CRC64;
                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                       375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR002181; -.
PFAM: PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                            GVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=ADRENAL CORTEX;
MEDLINE=98451564; PubMed=9776732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lab. Invest. 78:1385-1394(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF034699; AAC62490.1; -. AF032924; AAC78285.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42761 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 219-355 FROM N.A.
                                                                                                                                                                                                                                                                                                    ANGIOPOIETIN-2 (FRAGMENT).
                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272
                                                                                                                                                                                                                                                                                                                              taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  Q9TSKO;
                                                                                                                                                                                                                                                                                                                   ANGPT2 OR ANG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiogenesis
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CONFLICT
SEQUENCE
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                                        293
                                                                                                                                             412
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DB 6; Length 375;

Score 524.5; DE Pred. No. 3e-27;

22.1%; 34.2%;

Query Match Best Local Similarity

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14;
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                                                                                                                                                                                        119 VNNSVLQKQQHDLMETVNNLLTLMSTSNPSYSLLAKDEQI-----IFRDCGEAFKSG 170
                                                                                                                                                                                                                                                                                                                                                                      221 KRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRR 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPPLTIQLPRQFSRIEEVFKEVQNLKEIV--NSLKKSCQD-----CKLQADDNGDPGRNG 113
                                                                                                                                                       14 LLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGR-----LEK-LNLVN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 DALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 IMENNTOWLMKLENYIQDNMKKEMVEIQQNAVQN------QTAVMIEIGTNLLNQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 VLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEELEKKIVTATVNNSVLQKQQHDLMET 254
65; Gaps
                                                                                    22 LTDVEAQVLNQTTRL-----ELQLLEHSLSTNKLERQILLDQTSEISKLQ------DKNS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.0%; Score 523.5; DB 4; Length 495;
28.1%; Pred. No. 5e-27;
Live 76; Mismatches 155; Indels 125; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN 84
                                                                                                                                                                                                                                                                                                                                                                                                    135 TAEQTRKLTDVEAQVLNOTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK
                                                                                                                                                                                                                                                               166 MNNI----ENYVDSKVANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 EFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 MDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------LEKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Biologic significance of angiopoietin-2 expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K., Wands J.R.;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56848 MW; EBFAC35ABF1F08F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 NKFNGIKWYWKG-----SGY--SLKATTMMIRPADF 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 VR-NGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              495 AA.
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J. Clin. Invest. 103:341-345(1999).
EMBL; AB009865; BAA95590.1; -.
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58;
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15,
15,
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel.
01-0CT-2000 (TrEMBLrel.
01-0CT-2000 (TrEMBLrel.
ANGIOPOIETIN-2.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 NLV-----
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86 IMENNTQWLMKLENYIQDNMKKEMVEIQQNAVQN---
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
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                                                                                                                              Created)
                                               G-----SGY--SLKATTMMIRPADF 407
                                                                                                       PRT;
                                                                                                                                                                                                                                                                     MEDLINE=97349327; PubMed=9204896;
                        GVSEAHPGGYKSSFKEAKMMIRPKHF
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256
496
321
56919 MW;
                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 27.9%
Matches 138; Conservative
                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          Science 277:55-60(1997).
                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55
130
282
318
496 AA;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                 ANGIOPOIETIN-2.
                                                                                                                                                                                                                                                                                                                              angiogenesis.";
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MIM; 601922;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNRVRELESEVNKLSSELKNAKEEINVLHGR-----LEK-LNLVNMNNI-----ENYV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKRVLEMEDKHTLQLKSIKDEKDQLQVLVARQNSIIEELEKQLVTATVNNSVLQKQHDL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 DSKVAN-LTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHD 352
                                             METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
                                                                                                                                        DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                    LKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Gaps
                                                         163 METVHNLLTMISTPNSAKKNFIAKEEQIS:-----FKDCAEAFKSGLTTSGTYTLTFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 PKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLL
VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD
                                                                                          LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 NSAQEKKAYCDMESNGGGWTVLQRREGGSVDFHRTWKEYKIGFGDPAGEYWLGNEFVSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mezquita J., Mezquita B., Pau M., Mezquita C.; "Characterization of a novel form of angiopoietin-2 (Ang-2B) and expression of VEGF and angiopoietin-2 during chicken testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SEQUENCE 407 AA; 46647 MW; E10C03D07E410013 CRC64;
                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 523; DB 13;
Pred. No. 4.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 260:492-498(1999)
EMBL; AJ131923; CAB59200.1; -.
                                                                                                                                                                                                                                                                       407 AA.
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                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-HUBBARD WHITE MOUNTAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  development and regression."
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                                                                                                                                                                                                                                                                                                                             ANGIOPOIETIN-2B (ANG-2B).
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                                                                                                                                                                                                            482 -SLKATTMMIRPADF 495
                                                                                                                                                                                      423 SSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 TAEQTRKLTDVEAQVLNQTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --NMNNIENYVDSKVANLTF------V 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malsonpierre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J., Radžiejewski C., Compton D., McClain J., Aldrich T.H., Papadopoulos N., Daly T.J., Davis S., Sato T.N. Yancopoulos G.D.; "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATURATION: BINOLET MEDIATED BY ANGIOPOINTERACTS BLOOD VESSEL MATURATION/STABILITY MEDIATED BY ANGIOPOINTIN: (ANG-1). ITS FUNCTION MAY BE CONTEXT-DEFENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SICH AS VEGY, ANG2-MEDIAMED LOOSENING OF CELL-MATRIX CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR REGRESSION. IN CONCERT WITH VEGY. IT MAY FACILITATE ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE ANGIOGENIC SIGNAL SIGNAL SIGNAL ANGIOGENIC SIGNAL RELATED TO THE CTERMINAL PART OF THE BETA AND GAMMA CHAINS OF FIBRINGGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 MDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.0%; Score 522; DB 4; Length 496; 27.9%; Pred. No. 6.3e-27; ive 74; Mismatches 159; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLY.
5642A58847A7385C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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347 KHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NCI 405
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                                                                                                         406 FWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF
                                                                                                                                                                                                                                                                                                                            FIBRINGEN-LIKE PROTEIN 1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
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36.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.3%
Best Local Similarity 36.8%
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36378
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296
112
261
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70
83
248
312 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hirohashi S.;
                                                                                                                                                                                                                                                                  01-NOV-1996
                                                                                                                                                                                                                                                                                    01-NON-1096
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                                                                                                                       421
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                                                                                                                       METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
                                                                                                                                            LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
                                                                                                                                                                                                                                                                                    DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                                                                                                                                                                           SLKKSC------QDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELESEVNKLSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 KQQHDLMETVNNLLTMMSTSNSAKDPTVAKEEQIS-----FRDCAEVFKSGHTHNGI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 IMENNIQWIMKVLNQTTRLELQ-----LEHSLSTUKL-EKQILDQTSEINKLOD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGN 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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26 MDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LESRGKCE---EAGECPYQVSLPPL----TIQLPKQFSRIE-----EVFKEVQNLKEIVN 90
                                                                  VLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEELEKKIVTATVNNSVLQKQQHDLMET
                                       VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.;
"Characterization and expression of a novel alternatively spliced human anglopoietin-2.";
J. Biol. Chem. 275:18556-18556(2000).
EMBL; AFIBYBSS, AAF76526.1;
SEQUENCE 444 AA; 50958 MW; E512409CE73987A1 CRC64;
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Last sequence update)
Last annotation update)
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Pred. No. 7.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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29.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANGIOPOIETIN-2 ISOFORM-1.
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Best Local Similarity 29.6'
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                               423 SSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                        -SLKATTMMIRPADF 496
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"Molecular cloning and initial characterization of a novel fibrinogen-
related gene, HFREP-1.";
Blochem. Biophys. Res. Commun. 193:681-687(1993).
-!- SUBCELLULAR LOCATION: EXTRACELLULAR (PROBABLE).
-!- SUBCELLULAR LOCATION: EXTRACELLULAR (PROBABLE).
-!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
EMBL: D14446; BAA03336.1;
-HSSP; P02671; 1FZD.
366 QPGND----PSTKDGDNDKCIC-KCSQMLTGGWWFDACGPSNLNGMYYPQRQNTNKFNGI 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSLD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRG-VRNGIFWGTWPGVSEAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 OVRLLETRVKQQQVKIKQLLQE-----NEVQFLDKGDEDTVVD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBRINOGEN-LIKE PROTEIN 1.
BETA/CAMA CHAINS OF FIBRINOGEN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=HEPATOMA;
MEDLINE=93290661; PubMed=8390249;
Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,
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                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 13, Last annotation update)
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Pred. No. 3.7e-26;
; Mismatches 108;
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Plasma; Blood coagulation; Signal.
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                                                                                                                                                                                                                                       Kim I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.; "Molecular cloning and characterization of a novel angiopoietin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----IYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 TSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDPG 316
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.2%; Score 505; DB 4; Length 491; Best Local Similarity 26.9%; Pred. No. 8.3e-26; Matches 131; Conservative 81; Mismatches 137; Indels 138;
                                                                                                                                                                                                                                                                                                         INTERPRO; IPRO02181; -.
PFAM; PFO0147; fibrinogen_C; 1.
PROSTIE; PSO0514; FIBRIN_AG_C_DOMAIN; 1.
SEQUENCE 491 AA; 56719 MW; 3C4DB8DEF6CF7E99 CRC64;
                                                                                                                Last sequence update)
Last annotation update)
                                                                              491 AA.
                                                                                                     Created)
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MEDLINE=99148829; PubMed=10025962;
 GGYKSSFKEAKMMIRPKHFKP 439
              protein, angiopoietin-3.";
FEBS Lett. 443:353-356(1999).
EMBL; AF107253; AAD19608.1;
                                                                                                 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-2000 (TrEMBLrel. 13,
                                                                              PRELIMINARY;
                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                      SEQUENCE FROM N.A.
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4,83 VQMMIKP 489
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                                                                                                                                    ANGIOPOIETIN Y1
419
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49 VKELKAQVANLSSLLSELNKKQERDWVSVVMQVMELESNSKRMESRLTDAESKYSEMNNQ 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDP--KNSSFEVY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 IDIMQLQAAQTVTQTSADA----IY-DCSSLYQKNYRISGVYKLPPDDFLGSPELEVF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 CDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYY----HQKYRGVRNGIFWGTWPGVSEA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                   Homo sapiens (Human).
Buskryvota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.6%; Score 489; DB 4; Length 34 36.2%; Pred. No. 6.1e-25; ive 55; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                            Peek R., van Gelderen B.E., Bruinenberg M., Kijlstra A.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                  Bagguley C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Y16132; CAA76078.1; -.
EMBL; AL049653; CAB44734.1; -.
HSSP; P02671; 1FZD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO; IPR002181; -. PFAM; PF00147; fibrinogen_C; 1. SEQUENCE 346 Aa; 40018 MW; AEC0A601CC498B43 CRC64;
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Best Local Similarity 36.29
Matches 117; Conservative
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PRELIMINARY;
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01-MAY-2000
                  043827;
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DJ647M16.1.
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--EHKILEME---GKHKEELDTLKEEKENLQGLVTRQTYIIQELEKQL 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 LKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACL 385
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Eukaryota; Metazoa; Arthropoda; Chellcerata; Merostomata; Xiphosura;
Limulidae; Ταςhypleus.
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16 QKYGLTSSQNKE-----LCDVTSSTGLLDSIKVMASHVKEQLKDKGTSEVAQPIVSPDP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gokudan S., Muta T., Tsuda R., Koori K., Kawahara T., Seki N., Mizunoe Y., Wai S.N. Iwanaga S., Kawabata S.; "Horseshoe crab acetyl group-recognizing lectins involved in innate immunity are structurally related to fibrinogen."; Proc. Natl. Acad. Sci. US.A. 96:10086-10091(1999).
                                                                                                                                                                                        NLVNMNNIENYVDSKVANLTFVVNSLDGKCSK----CPSQEQIQSRPVQHLIYKDCSDYY
                                                                  238 NRATTNN--SVLQKQQLELMDTVHNLVNLCTKEGVLLKGGKREEEKP----FRDCADVY
                                                                                                  AIGKRSSETYRV----TPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKA
                                                                                                                                                                       GFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVG
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PFAM; PF00147; fibrinogen_C; 1.
PROSTIE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SEQUENCE 292 AA; 33786 MW; D028DE1E2716F71A CRC64;
                                                                                                                                                                                                                                                                                                         394 YHQ-KYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
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Last annotation update)
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; Pred. No. 8.4e-25;
49; Mismatches 104;
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Best Local Similarity 36.38
Matches 106; Conservative
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 192 SLL----
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A Medline=96051389; PubMed=7584028;

A Medline=96051389; PubMed=7584028;

A Medline=96051389; PubMed=7584028;

A Sato S., Nagase T., Seki N., Ishikawa K.I., Tabata S.;

The coding of the coding sequences of unidentified human genes. I.

The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid recall line KG-1 (supplement).";

DNA Res. 1:47-56(1994)

TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A CRUCIAL ROLE IN MEDIATION RECIPROCAL INTERACTIONS BETWEEN THE COMPANY AND MESCHPOCAL INTERACTIONS BENDEATES BLOOD WESSEL MATURATION/STBAILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANDOUS: IT MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE
IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR
PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
                        TISSUE-FETAL LUNG;
MEDLINE-97134663; PubMed-8980223;
Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
Ryan T.E., Bruno J., Radzlejewski C., Maisonpierre P.C.,
                                                                                                                                                                              MEDLINE=96051387; PubMed=7584026;
MEDLINE=96051387; PubMed=7584026;
Nomura N., Miyajima N., Szauka T., Tanaka A., Kawarabayashi Y.,
Nomura N., Miyajima N., Ishikawa K.-I., Tabata S.;
"Prediction of the coding sequences of unidentified human genes. I.
The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---RLEK-L 161
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
5D5FA63AEF6BE920 CRC64;
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                                                                                                                  "Isolation of angiopoietin-1, a ligand for the TIE2 receptor,
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COLLED COIL (POTENTIAL).
FIBRINGEN BETA/GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 LTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLLQQTNEILKIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 GLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 1.4e-24; 59; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Glycoprotein; Coiled coil.
                                                                                                                                  secretion-trap expression cloning.";
Cell 87:1161-1169(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U83508; AAB50557.1; -. D13628; BAA02793.1; -. P02671; 1FZD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.5%;
32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLY DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                         DNA Res. 1:27-35(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002181; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISCHEMIC HEART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243
295
498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                       cell line KG-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                    related protein. angiopoietin-related protein induces endothelial cell sprouting.";
                                                                                                                                                                                                                                                                                                                                                                                         LQLASKYKDLEHKFQHLAMLAHNQSEVIAQLEEHCQRV------PAARPMPQPPPAA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417
                                                                                                                                                                                                                                                                                                                                                                     IQLPKQFSRIEEVFKEV --- QNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGA 121
                                                                                                                                                                                                                                                                                                                                                                                                              PGEVGD----NRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKV 177
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                              MEDLINE=99403103; PubMed=10473614;
Kim I., Moon S.O., Koh K.N., Kim H., Uhm C.S., Kwak H.J., Kim N.G.
Koh G.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPRVYQPPTYNRI-----INQISTNEIQSDQNLKVLPPSLPTMPAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 ANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 FEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYY ---HQKYRGVRNGIFWGTWPGVS
                                                                                                                                                                                                                                                                                                                                                  73;
                                                                                                                                                                                                                                                                                                                               DB 11; Length 493
                                                                                                                                                                                                                                                                                                                             ; Score 485.5; DB 11; Length; Pred. No. 1.6e-24; 62; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                22885ABEF0746BF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ANGIOPOIETIN-RELATED PROTEIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
                                      493 AA
                                                                                                                                                                                                                                                                INTERPRO; IPRO02181; -.
PROMIP PF00147; fibrinogen_C; 1.
PROSTIF: PROSTIF: FIBRIN_AG_C_DOMAIN; 1.
SEQUENCE 993 AA; 57118 WW; 22885ABEF
                                                                                                                                                                                                                                    Biol. Chem. 274:26523-26528(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAHPGGYKSSFKEAKMMIRP 434
                                                                                                                                                                                                                                                                                                                              20.4%;
30.8%;
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04,
15,
                                                                                                                                                                                                                                    J. Biol. Cnem. 2...
EMBL; AF125176; AAD55358.1;
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 30.8%
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | |: |||||
----GSY---SLKKVVMMIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  008538;
01-JUL-1997 (TYENBLED: 04
01-JUL-1997 (TYENBLED: 04
01-OCT-2000 (TYENBLED: 15
ANGIOPOIETIN-1 (ANG-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                     PRELIMINARY;
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=10090;
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008538
1D 008538
AC 008538,
DT 01-0CT
DT 01-0CT
DE ANGIOP
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                                      09R045
                                                09R045
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                  RESULT
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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQ- 396
                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING TIE2 TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 GLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGR-----LEKLNLVN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 TAGKQSSLILH-GAD---FSTKDADNDNCMC-KCALMLTGGWWFDACGPSNLNGMFYTAG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71; Gaps
                                                                                                                                                                                                                     MEDLINE=97134663; PubMed=8980223;
Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain
Ryan T.E., Bruno J., Radziejewski C., Maisonpierre P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COILED COIL (POTENTIAL).
FIBRINGEN BETA/GAMMA.
N-LINKED (GLCNAC. . .) (POTENTIAL).
AM, 28584FDECZ60D800 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 SLL------EHKILEMEGKHKEELDTLKEEKENLOGLVSRQTFIIQELEK-QLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 ATNNNSILQKQQLELMDTVHNLVSLCTKEGVLLKGGKREEERP-----FRDCADVYQAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 LTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLLQQTNEILKIHE------KN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 MNNIENYVDSKVANLTFVVNSLDGKCSK----CPSQEQIQSRPVQHLIYKDCSDYYAIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 RSSETYRV----TPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 LRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATION WITH ENDOTHELIAL CELLS.
SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART
THE BETA AND GAMMA CHAINS OF FIBRINGGEN.
P. U83509; AAB50558.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.3%; Score 483.5; DB 11; Length 498; 31.7%; Pred. No. 2.2e-24;
                                                                                                                                                                                                                                                                                                                                                 a ligand for the TIE2 receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM: PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Glycoprotein; Coiled coil.
                                                                                                                                                                                                                                                                                                                       Yancopoulos G.D.;
"Isolation of anglopoietin-1, a li
secretion-trap expression cloning.
Cell 87:1161-1169(1996).
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M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:108448; Agpt.
INTERPRO; IPR002181; -
ANGPT1 OR AGPT.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
295
498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                              Mammalia; Eutheri
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Search completed: February 27, 2001, 12:49:35 Job time: 120 sec

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GenCore version 4.5
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	; Search time 30.15 Seconds (without alignments) 497.880 Million cell updates/sec	GYKSSFKEAKMMIRPKHFKP 439	
OM protein - protein search, using sw model	February 27, 2001, 12:47:35; Search time 30.15 Seconds (without alignments) 497.880 Million cell update	US-09-442-143-2 2378 1 MKLANWYWLSSAVLATYGFLGYKSSFKEAKMMIRPKHFKP 439	BLOSUM62 Gapop 10.0 , Gapext 0.5
OM protein - pr	Run on:	Title: Perfect score: Sequence:	Scoring table:

268485 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

268485 seqs, 34193795 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1987. /SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1993.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:* A_Geneseq_36:* Database :

/SIDS1/gcgdata/geneseq/geneseqp/AA1994.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1996.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human prothrombina Rat hepatic parenc Human TIE-2 ligand Human TIE-2 ligand Human TIE-2 ligand Human anglopoietin Human anglopoietin Amino acid sequenc Amino acid sequenc Hepatocyte prolife Hepatocyte prolife
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SUMMARIES	335 335 335 335 335 335 335 335 335 335
SU	W88236 W88235 W88236 R65759 W01411 R94605 W47532 Y78903 Y78906 W47529 W47529 W47529
DB	20 20 17 17 19 19 17
Length	4484444446 8884666666666666666666666666
\$ Ouery Match Length DB	100.0 77.9 22.0 22.0 22.0 22.0 22.0 22.0 22.0 22
Score	2378 1853.5 524 522 522 522 522 522 521 517.5 505.5
Result No.	100 8 8 9 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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W88235 standard; Protein; 439 AA (first entry) 15-MAR-1999 W88235; RESULT W88235

ALIGNMENTS

Human prothrombinase Fg12 protein.

Prothrombinase, hfg12, Fg12, human, immune coagulation, antibody, inhibitor, infection, graft rejection, glomerulonephritis, cancer; gastrointestinal disease, foetal loss, therapy, vaccine.

			Location/Qualifiers	179183	/label= Asn is N-glycosylated	235238	/note= "Asn is N-glycosylated"	262265	/note= "Asn is N-qlycosylated"	336337	/note= "Asn is N-glycosylated"	213439	/note= "fibrinogen related domain"	364378	/note= "epitope (Claim 4)"
	Homo saptens.		Key	Modified-site		Modified-site		Modified-site		Modified-site		Domain		Peptide	
4	SO	XX	FН	FT	ΡŢ	FT	FŢ	FT	FŢ	FT	FŦ	FJ	FI	FT	FT

15-MAY-1998; · 98WO-CA00475. 19-NOV-1998. XXXXXX

W09851335-A1.

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inhibitor; infection; graft rejection; glomerulonephritis; cancer; gastrointestinal disease; foetal loss; therapy; vaccine.
                                                                                              Prothrombinase; Fg12; mouse; immune coagulation; antibody;
                                                                         Mouse prothrombinase Fg12 protein.
          W88236 standard; Protein; 432 AA
                                                    15-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    (LEVY/) LEVY G
                                                                                                                                                             Key
Modified-site
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15-MAY-1997;
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                               W88236;
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 W88236
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                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                             This is the amino acid sequence of human prothrombinase Fgl2, as predicted from hfgl2 DNA (see V84139). Fgl2 is a 70 kDa transmembrane serine protease that has immune procoagulant activity. The invention provides a method for inhibiting immune coagulation by
                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVS 60
                                                                                                                                                                                                                                                                 allograft and xenograft rejection and foetal loss. An Fg12-specific
                                                                                                                                                                                                                      inhibiting the activity or expression of Fgl2. The method can be used in Nivo to treat a condition which requires a reduction in immune coagulation such as bacterial and viral infections, cancer, glomerulonephitits, a number of gastrointestinal diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL
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                                                                                                                immune coagulation - by using Fg12 antibodies and used to treat conditions including graft rejection and
                                                                                                                                                                                                                                                                           antibody, an Fg12 antisense oligonucleotide, or a substance that affects prothrombinase activity of a Fg12 protein may be used to treat a condition requiring a reduction in procoagulant activity. A vaccine containing an Fg12 protein or peptide is used for prevention of graft rejection or foetal loss (claimed).
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                                                                                                                                                          Claim 8; Page 66-67; 105pp; English.
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         97US-0061684.
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                                                                                 WPI; 1999-059687/05
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Best Local Similarity
Matches 439; Conserv
                                                                                                                                                                                                                                                                                                                                         439 AA;
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                                         (LEVY/) LEVY G.
                                                                                              N-PSDB; V84139
         10-OCT-1997;
                   15-MAY-1997;
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                                                                                                                           compounds,
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                             Levy G;
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/note= "fibrinogen related domain"

98WO-CA00475 97US-0061684 97US-0046537

"Asn is N-glycosylated"

/note= "A 213..439

/note= "Asn is N-glycosylated" 323..325 /228..231 /note= "Asn is N-glycosylated"

/label= Asn is N-glycosylated

Location/Qualifiers 172..174

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Gaps
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                                                                                                                                                                                                                                                                        Modulating immune coagulation - by using Fg12 antibodies and compounds, used to treat conditions including graft rejection and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is the amino acid sequence of mouse prothrombinase Fgl2, as
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WPI; 1999-059687/05.
                                                                                                 N-PSDB; V84140.
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1 MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVS 60

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Human TIE-2 ligand 2.
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                                                 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG 120
                                                                                                                   APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL 180
                                                                                                                                                                                                                                                           YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300
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TFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatic parenchymal cell growth promoter peptide - is isolated from human or animal liver cell or produced by recombinant techniques and used for therapy of liver diseases
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liver cancer; cirrhosis.
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1..24
/label= sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R65759 standard; protein; 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350
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The protein or the N-terminal peptide (R65758) may be used in the diagnosis and treatment of liver diseases, such as liver cancer and cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIE-2 ligand 2; tyrosine kinase with Ig and EGF homology domain; receptor; antagonist; neovascularisation; wound healing; ischaemia; leukopaenia; thrombocytopaenia; anaemia; angiogenesis; tumour; atherosclerosis; inflammation; diagnosis; therapy.
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                                                                                                                                                                                                              26;
                                                                                                                                                                 Length 314;
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                                                                                                                                                               22.0%; Score 524; DB 15; 137.6%; Pred. No. 4.3e-39; ive 46; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIE-2 agonists and antagonists and related DNA promoting or blocking neovascularisation, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldfarb M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410 WPGVSEAHPGGYKSSFKEAKMMIRPKHFKP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aldrich TH, Bruno J, Davis S,
Maisonpierre PC, Radziejewski C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
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WO9611269-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        imenntqwlmklenyiqdnmkkemveiqqnavqn-----qtavmieigtnllnq 134
                                                                                                                                                                                                                           26 mdsigkkqyqvqhgscsytfllpemdncrsssspyvsnavqrdapleyddsvqrlqvlen 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anglogenesis; neovascularisation; tumour development; wound healing; TIE; tyrosine kinese with 1g and EGF homology domains; vector; recombinant; clone; diagnosis; ischaemia; thromboembolytic disease; atherosclerosis; inflammation; diabetes; ligand bodies; delivery;
                                                                                                                                                                                                       LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN 84
                   Human TIE-2 (tyrosine kinase with Ig and EGF homology domains)
ligand 2 (W01411) is a ligand that binds the TIE-2 receptor. Its
amino acid sequence was deduced from a cDNA clone (744321) derived
from human foetal lung cells. TIE-2 ligand 2 is a receptor
antagonist useful for blocking blood vessel growth, for tumour
therapy and for treating a proliferative disorder of a blood-
forming organ. It can be obtd. from natural sources or expressed
in transformed host cells.
                                                                                                                                                                                                                                                                                                                                                                195 vlamedkhiiqlqsikeekdqlqvlvskqnsiieelekkivtatvnnsvlqkqqhdlmet
                                                                                                                                                                                                                                                                                                                                                                                                     METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID
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                                                                                                                                                         22.0%; Score 522; DB 17; Length 496; 27.9%; Pred. No. 1.3e-38; 1.1ve 74; Mismatches 159; Indels 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TIE-2 ligand 2 derived from pBluescript KS clone.
                                                                                                                                                                                                                                                                                                                                           ---NMNNIENYVDSKVANLTF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R94605 standard; Protein; 496 AA.
Claim 15; Fig 6; 113pp; English.
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                                                                                                                                                                                 Conservative
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                                                                                                                                                                     Local Similarity
nes 138; Conserv
                                                                                                                           496 AA;
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R94605 is a human TIE-2 (hTIE-2) ligand 2 derived from a pBluescript KS clone. hTIE-2 ligand DNAs of the invention are recombinant versions of the native ligand coding sequences and may be used to produce the ligands at a high yield. Antibodies and receptor bodies that bind to TIE-2 ligands may be used to inhibit angiogenesis and neovascularisation temeselves are useful to promoche percept and the TIE-2 ligands. Tierat thromochembolytic dischaemia. TIE-2 ligands are also useful to promoche neovascularisation and wound healing e.g. for treatment of ischaemia. TIE-2 ligands are also useful to tireat thromochembolytic disease, atheroselerosis, inflammation and diabetes. Ligand bodies contq. TIE-2 ligands may also be useful for the delivery and targeting of growth factors, toxins etc. to sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 taeqtrkltdveaqvlnqttrlelqllehslstnklekqildqtseinklqdknsflekk 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding TIE-2 ligand and related vectors - useful in diagnosis and treatment of neovascularisation, tumours, etc., or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----RVRELESEV-----LEKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.0%; Score 522; DB 17;
27.9%; Pred. No. 1.3e-38;
tive 74; Mismatches 159
                                                                                                                                                                                                                                                                                                                                                                       Goldfarb M,
Yancopoulos
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PC, Radziejewski C,
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                                                                                                                                       94US-0319932.
94US-0330261.
94US-0348492.
94US-0353503.
95US-0373579.
                                                                                                            95US-0418595
                                                       95WO-US12935
                                                                                                                                                                                                                                                                                                                  (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         promote wound healing, etc.
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les 138; Conserv
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                                                                                                                                                                 27-OCT-1994;
02-DEC-1994;
09-DEC-1994;
17-JAN-1995;
                                                       06-OCT-1995;
18-APR-1996
                                                                                                               06-APR-1995
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98US-0110600
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                          -----RVRELESEV-
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-slkattmmirpadf
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N-PSDB; 292213.
                                                                                                                           162 NLV----
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02-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of the human TIE-2 ligand 2, used in the method of the invention, involving the production of TIE-2 ligands which promote healing. The nucleic acids, vectors and host calls used in the method of the invention are useful for the recombinant production of the ligands. The ligands, etc. are useful for blocking blood vessel growth, promoting neovascularisation, promoting the growth or differentiation of a cell expressing the TIE receptor, blocking the growth or differentiation of a cell expressing the TIE receptor and for attenuating or preventing tumour growth in
                  375 lkdwegneayslyehfylsseelnyrihlkgltgtagkissisqpgnd----fstkdgdn 430
                                                                                                                      431 dkcic-kcsqmltggwwfdacgpsnlngmyypqrqntnkfngikwyywkg-----sgy- 482
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                                                                       DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK
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llarity 27.9%; Pred. No. 1.3e-38;
Conservative 74; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human TIE-2 ligand 2 from clone pBluescript KS.
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96US-0022999
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Best Local Similarity
Matches 138; Conserv
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sequence. Ang-2 is a naturally occurring angiogenesis antagonist when vascular endothelial growth factor (VEGF) levels are low, and generally counteracts the blood vessel maturation and stability mediated by Ang-1. Ang-1 is a naturally occurring angiogenesis agonist, and is a maturation or stabilisation factor, converting immature vessels to mature vessels.
                                                                                                           243
taeqtrkltdveaqvlnqttr1elq11ehs1stnk1ekqi1dqtseink1qdknsf1ekk 194
                                   183
                                                                       195 vlamedkhiiqlqsikeekdqlqvlvskqnsiieelekkivtatvnnsvlqkqqhdlmet 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiopoietin-2; Ang-2; vascular endothelial growth factor; tumour; vascularisation; angiogenesis; blood vessel maturation; malignant; benign; binding ligand; cancer; aminophospholipid.
                                                                                                           184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD
                                                                                                                                             255 vnnlltmmstsnsakdptvakeeqisfrdcaevfksghttngiytltfpnsteeikaycd
                                                                                                                                                                                                       304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN
                                                                                                                                                                                                                                                                             ----NMNNIENYVDSKVANLTF---
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Both Ang-1 and Ang-2 are useful in a therapeutic approach to the treatment of vascularised tumours. The invention relates to a binding ligand comprising a targetling agent that binds to an aminophospholipid, linked to a therapeutic agent (e.g. Ang-2). Aminophospholipids are stable and specific markers accessible on the luminal surface of tumour blood vessels. The binding ligand induces coagulation (thrombosis) in tumour vasculature or causes tumour necrosis (possibly by cell- or complement-mediated cytocoxicity and/or apoptosis). The binding ligands are used to treat vascularised tumours, malignant or benign, in animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; angiopoietin-2; Ang-2; aminophospholipid; vascularised tumour;
unconjugated anti-aminophospholipid antibody; tumour blood vessel marker;
cancer; treatment; angiogenesis.
                                                                                                                                                                                                                                                                                                                  -----NKLSSELKNAKEEINVLHGR---LEKL 161
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135 taeqtrkltdveaqvlngttrlelgllehslstnklekgildgtseinklgdknsflekk 194
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                                                                                                                                                                      22.0%; Score 522; DB 21; Length 496; 27.9%; Pred. No. 1.3e-38; ive 74; Mismatches 159; Indels 12
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                                                                                                            especially large tumours.
                                                                                                                                                                                              Conservative
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-slkattmmirpadf 496
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                                                                                                                                                                      Query Match
Best Local Similarity
Matches 138; Conserv
                                                                                                                                    496 AA;
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This sequence represents the human angiopoietin-2 (Ang-2) amino acid sequence. Ang-2 is a naturally occurring angiogenesis antagonist when vascular endothelial growth factor (VBGF) levels are low, and generally counteracts the blood vessel maturation and stability mediated by Ang-1.
Ang-1 is a naturally occurring angiogenesis agonist, and is a maturation or stabilisation factor, converting immature vessels to mature vessels. Both Ang-1 and Ang-2 are useful in a therapeutic approach to the treatment of vascularised tumours. The invention relates to a composition comprising an anti-mainophospholipid antibody, or its antigen binding region. The composition is used to kill tumour vasculature endothelial cells. Aminophospholipids are stable and specific markers accessible on the luminal surface of tumour blood vessels. Ang-1 or Ang-2 may be used malignant or benign vascularised tumours in animals, especially large
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195 vlamedkhiiqlqsikeekdqlqvlvskqnsiieelekkivtatvnnsvlqkqqhdlmet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 mdsigkkqyqvqhgscsytfllpemdncrsssspyvsnavqrdapleyddsvqrlqvlen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 522; DB 21; Length 496;
; Pred. No. 1.3e-38;
74; Mismatches 159; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 NLV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 223-224; 226pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.0%; Score 522; 27.9%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 LESRGKCE---EAGECPYQVSLPPL----
                                                                     98US-0092672.
99WO-US15600
                                                                                                                                                                              (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                     WPI; 2000-182175/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496 AA;
                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Z92215
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12-JUL-1999;
                                                                     13-JUL-1998;
02-DEC-1998;
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218 AIGKRSSETYRVTPDPKNSSFEVYCDMĒTMGGGWTVLQARLDGSTNFTRTWQDYKAGFGN
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96US-0022999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yancopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-145615/13.
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Matches 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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02-AUG-1996;
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                    431 dkcic-kcsqmltggwwfdacgpsnlngmyypqrqntnkfngikwyywkg-----sgy- 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 ltdvetgvlngtsrleigllenslstyklekgllggtneilkihe-------kn 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 sll-----ehkileme---gkhkeeldtlkeekenlgglvtrqtyiigelekgl 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLVNMNNIENYVDSKVANLTFVVNSLDGKCSK----CPSQEQIQSRPVQHLIYKDCSDYY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 GLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHG------RLEK-L 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified human TIE-2 receptor ligand(s) - useful for promoting wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71;
                                                                                                                                                                                                                                                                                                                              Amino acid sequence of chimeric TIE ligand INIC2F (chimera 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 498;
                                                                                                                                                                                                                                                                                                                                                                      Chimeric TIE ligand 1N1C2F; TIE-2 ligand; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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1; Mismatches 138;
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                                                                                                                                                                                                    W47528 standard; Protein; 498
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32.7%;
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                                                                                   | | | ||||| |
483 -slkattmmirpadf 496
                                                            423 SSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yancopoulos
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Best Local Similarity
Matches 131; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                       410
                                                                                                                                                                                                                                                               397
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TAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQK
                                                                                      LRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNG
                                                                                                                               |:||||: : || : :|:| |:|: | |:|:| ||:|: || psgeywlgnefvsgltnqqryvlkihlkdwegneayslyedfylsseelnyrihlkgltg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of chimeric TIE ligand 1N2C2F (chimera 3).
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                                                                                                                                                                                                                                                                                                                                                            398 YRGVR-NGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                     3.4e-38;
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Vector for expression of hepatocyte proliferation substance
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                                                                                                                                                                                                                                                                                                                                                                   probe; SR-alpha promoter;
                             qvlvskqnsiieelekkivtatvnnsvlqkqqhdlmetvnnlltmmstsnsakdptvake 279
                                                                                                                                                                    ehdgncresttdgyntnalgrdaphvepddsvgrlqvlenime--nntgwlmklenyigd 106
                                                                                      ----NMNNIENYVDSKVANLTF------VVNSLDGKCSKCPSQEQIQSRPV 205
                                                                                                                         QHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFT 265
                                                                                                                                                                                             LKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACL 385
                                                                                                                                                                                                             400 lnyrihlkgltgtagkissisqpgnd----fstkdgdndkcic-kcsqmltggwwfdacg 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vector for expression of hepatocyte proliferation substance - in eukaryotic cells, used as diagnostic reagent for hepatitis and for basic research on in vitro liver cell cultures
                                                                                                                                  RTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEF
                  SCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN------RVRELESEV----
                                                                    160 elgllehslstnklekgildgtseinklgdknsflekkvlamedkhiiglgsikeekdgl
                                                                                                                                                                                                                                            SANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
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                                                    -------KLSSELKNAKEEINVLHGR---LEKLNLV--
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                                                                                                                                                                                                                                                                                                                                                                 Human hepatocyte proliferation substance, r
chinese hamster ovary cell; CHO; hepatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                     1..22
/note= "signal peptide"
23..312
/note= "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                               (first entry)
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N-PSDB; T13397.
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                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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This is the amino acid sequence of a variant human hepatocyte proliferation substance (HPS). The variant differs from the sequence encoded by T13396 at pos. 214: A to G change and pos. 314: T to C. These changes alter the amino acid residues at pos. 50 of the mature protein: lie to Val and pos. 83: Leu to Pro. The gene was isolated from a lambda-gt10 human cDNA library using the sequence T13396 as a probe. The human gene was cloned in plasmid pSCL to produce plasmid pSVLH which was subsequently recombined to produce plasmid pCDLH-dhfr in which the HSS gene is under control of the SR-alpha promoter. This plasmid is transformed into CHO cells to express the HPS protein. The HPS protein can be used to diagnose hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human hepatocyte proliferation substance; rat; probe; SR-alpha promoter; chinese hamster ovary cell; CHO; hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYKAGFGNL---RREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 YKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYRLHVGNYNGTAGDALRFNKH----YNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 FDACLSANLNGKYYHQKYRG-VRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHFKP
                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                     Length 312;
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                                                                                                                                                                                                                                                                                                                                                                                                                    88;
                                                                                                                                                                                                                                                                                                                                                                  21.3%; Score 506; DB 17;
44.6%; Pred. No. 1.8e-37;
ive 25; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatocyte proliferation substance HP-041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shindo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R94316 standard; Protein; 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94JP-0228234.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-JP01904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23..312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-188445/19
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                               Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-1996
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                                                                                                                                                                                                                                                                                                  Sequence
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/label= Immunogen
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Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 AA;
                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holloway JL,
                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-1998;
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Best Local &
                                  Peptide
                                                                       Peptide
                                                                                                           Peptide
                                                                                                                                                Domain
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                                                                                                                                                                                                                                                           10;
                                                                 This is the amino acid sequence of a human hepatocyte proliferation substance (HPS). The gene encoding the HPS was isolated from a lambda-gtl0 human cDNA library using a fragment of the corresp. rat gene as a probe (sequence not given in the specification). The human gene was cloned in plasmid pSCL to produce plasmid pSVLH which was subsequently recombined to produce plasmid pSVLH which the HPS gene is under control of the SR-alpha promoter. This plasmid is transformed into CHO cells to express the HPS protein. The HPS protein can be used to diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human zapo3 protein; angiopoietin-1; angiopoietin-2; covalently linked; moiety; affinity tag; toxin; radionuclide; enzyme; fluorophore; multimer; coiled coil domain; carboxyl-terminal fibrinogen-like domain; angiogenic; haematopoietic; mitogenic activity; angiogenesis; inhibitor; endocrine-vascular cell association; revascularisation; DNA probe;
                                                                                                                                                                                                                                                                                                                                                                                                      117 -gggwtvigrrsdgsenfnrgwkdyengfgnfvqkhgeywlgnknlhflttqedytlkid 175
                                                                                                                                                                                                                                                                                 131 RELESEVNKLSSELKNAKEEINVLHGRLE----KLNLVNMNNIENYVDSKVANLTFVVNS 186
                                                                                                                                                                                                                                                                                                                                                          ----skrq----yadcseifndgyklsgfykikplqslaefsvycdmsd 116
                                                                                                                                                                                                                                                                                                                                                                                 247 MGGGWTVLQARLDGSTNFTRTWQDYKAGFGNL---RREFWLGNDKIHLLTKSKEMILRID 303
                                                                                                                                                                                                                                                                                                                                                                                                                                 304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKH-----YNHDLKFFT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                               358 TPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRG-VRNGIFWGTWPGVSEA 416
                                                                                                                                                                                                                                                                                                          75
        eukaryotic cells, used as diagnostic reagent for hepatitis and for
                                                                                                                                                                                                                                                                                                         18 rei-saledcaqeqmrlraqvrlletrvkqqqvkikqllqenevqfldkgdentvidlg-
                                                                                                                                                                                                                                                                                                                                 187 LDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 twdrdhdny-egncaeedqsgwwfnrchsanlngvyysgpytaktdngivwytw----
                                                                                                                                                                                                                                                          45;
                                                                                                                                                                                                                                Length 312;
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "For production of antibodies"
93..98
                                                                                                                                                                                                                                Score 505.5; DB 17;
Pred. No. 2e-37;
0; Mismatches 119; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..21
/label= Secretory_Signal_Sequence
                    in vitro liver cell cultures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuronal degeneration; anti-zapo3 antibody
                                           Page 23-24; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogen
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                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y26196 standard; Protein; 491
                                                                                                                                                                                                                                21.3%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 HPGGYKSSFKEAKMMIRPKHFKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                          Conservative
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/label- i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human zapo3 protein.
                                                                                                                                                                                                                                             Best_Local Similarity
Matches 119; Conserv
                    basic research on
                                                                                                                                                                                              312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-NOV-1999
                                                                                                                                                                       hepatitis.
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                  Query Match
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15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a human zapo3 protein. Zapo3 protein exhibits
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human angiopoietin homologue, ZAPO3 useful for study and regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKCEEAGECPYQVSLPPLTIQLP-----KQFSRIEEVF--KEVQNLKEIVNSLKKSCQ
                                                                                                                                                                                                                                                                                                                                     631-864 of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Amino-terminal_coiled_coil_domain
"For production of antibodies"
                                                /label= Immunogen
/note= "For production of antibodies"
                                                                                                                                                                                                                        /label= Immunogen
/note= "For production of antibodies"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Conserved cysteine residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Conserved cysteine residue"
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Pred. No. 4.4e-37;
                                                                                                                                                                                                                                                                                                                               /note= "Homologous to residues
fibrinogen alpha chain "
                                                                                                                                                                                                                                                                                                     /label= Fibrinogen-like_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Conserved cysteine 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Conserved cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                /label= Immunogen
/note= "For production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 65-67; 78pp; English.
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26.9%;
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                            125
                                                                                                            421..426
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  /note=
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Human TIE ligand; NL1; NL4; NL5; NL8; Ig homology domain; angiogenesis; EGF homology domain; receptor tyrosine kinase; vascular endothelial cell; early haemopoiestic cell; haemopoiestis; neconscularisation; wound healing; endothelial cell; growth inhibitor; apoptosis inducer; tumour cell; vasculogenesis; detection; diagnosis; therapy.
                                                                                                                                 316
                                                                                                                                                                  --ivnevkllrkesrnmnsrvtglymg 136
                                                                                                                                                      GWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNG 309
                                                                                                                                                                                                                                            NCGLYYSSGWWFDACLSANLNGKYYH-QKYRGV-RNGIFWGTWPGVSEAHPGGYKSSFKE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                  -------IYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGG
                                                                                                                         VELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSG
                                                                                                                                                                                                             This sequence is the human tyrosine kinase containing Ig and EGF homology domains (TIE) ligand of the invention, designated NLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated TIE ligand homologs for, e.g. developing products treatment of tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski PJ, Gurney AL;
D;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human TIE ligand NL5 protein sequence.
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                                                                DGKCSKCPSQEQIQSRP-----VQHL-
                      L----EKLNLVNMNNIENYV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roy M,
                                                                                                                                                                                                                                                                                                    :|||:|
483 vqmmikp 489
                                                                                                                                                                                                                                                                                        AKMMIRP 434
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the TIE receptors are receptor tyrosine kinases which are expressed in vascular endothelial cells and early haemopoietic cells. The TIE receptors are believed to be actively involved in anglogenesis, and may play a role in haemopoiesis as well. The TIE ligand homologs can promote the survival and/or growth and/or differentiation of TIE receptor expressing cells. They can be used for promoting neovascularisation in wound healing and for promoting anglogenic processes, such as for inducing collateral vascularisation in an ischaemic heart or limb, or for promoting bone development and/or maturation and/or growth in a patient or muscle growth and development. The TIE ligand homologs and antibodies can inhibit the growth of endothelial cells and induce apoptosis of cells, particularly tumour cells. They can inhibit vascularisation of tumour cells. The antibodies can also inhibit vascularisation of a cell in which a gene encoding an NIJ, NIS, NIB or NIA polypeptide is amplified. The products can also be used for antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 llheiirkrdnslelsglenkilnvttemlkmatryrelevkyasltdlvnngsvmitll 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||| | | | ::|: | | | 357 tsptkspfkippvtfinegpfkdcqqakeaghsvsgiymikpensngpmqlwcensldpg 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 VELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 kkvyaeyssfrlepesefyrlrlgtyggnagdsmmw----hngkgfttldrdkdmy-ag 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 NCGLYYSSGWWFDACLSANLNGKYYH-QKYRGV-RNGIFWGTWPGVSEAHPGGYKSSFKE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 DCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGR 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 GKCEEAGECPYQVSLPPLTIQLP-----KQFSRIEEVF--KEVQNLKEIVNSLKKSCQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 eeqclrifsrqdthvspplvqvvpqhipnsqqytpgllggneiqrdpgyprdlmpppdla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 20;
4.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.2%; Score 505; DB 26.9%; Pred. No. 4.4e-tive 81; Mismatches
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Matches 131;
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Best Local S
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us-09-442-143-2.rag

e.g. cardiovascular disorders, cell proliferative disorders, autoimmune and inflammatory disorders, and reproductive disorders. HANG antibodies and polynucleotides are useful for diagnosis of diseases associated with expression of HANG.

491 AA;

Sequence

8888888

Query Match

Length 491;

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proliferative disorder; autoimmune disorder; inflammatory disorder;
                                                                                                                                                                                                                                                            "potential casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                       "potential casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                     site"
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                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "potential tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                      "potential tyrosine kinase phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide useful for diagnosing, treating or preventing cardiovascular, cell proliferation, autoimmune/inflammatory, and reproductive disorders comprises amino acid sequence encoding human
                                                                                                                                                                                                                                                                                                                                                   "potential casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                          "potential casein kinase II phosphorylation
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                                                                                                                                                         "cAMP and cGMP-dependent protein kinase
                                                                                                                                                                                                                "potential glycosylation site"
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                                                                                                                                                                     phosphorylation site"
                                                                           /note= "signal peptide"
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                                                       Location/Qualifiers
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                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2000
                                                         Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
cell
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The present sequence represents a human angiopoietin (HANG) polypeptide. Nucleic acids encoding HANG were first identified in Incyte Clone 2365223 from an adrenal tissue cDNA library. The HANG polypeptide, and HANG antagonists are useful for treating or preventing a disorder associated with decreased or increased HANG expression or activity,

Claim 1; Fig 1A-F; 73pp; English.

angiopoietin

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15;
                                                                                                                                                                                                                                                                                                                          376
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                                                                                                                                                                                                                                                                                                                                                                                                     NCGLYYSSGWWFDACLSANLNGKYYH-QKYRGV-RNGIFWGTWPGVSEAHPGGYKSSFKE 427
                          Gaps
                                                  47 GKCEEAGECPYQVSLPPLTIQLP-----KQFSRIEEVF--KEVQNLKEIVNSLKKSCQ
                                                                                                                                                   L-----EKLNLYNMNNIENYV----------DSKVANLTFVVNS-----L
                                                                                                                                                                                                                                                                                                                -----ivnevkllrkesrnmnsrvtqlymq
                                                                                                                                                                                                                                                  -----IYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGG
                                                                                                                                                                                                                                                                       257 tsptkspfkippvtfinegpfkdcqqakeaghsvsgiymikpensngpmqlwcensldpg
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                                                                                                                                                                                                                                                                                                                                                                 eeqclrifsrqdthvspplvqvvpqhipnsqqytpgllggneiqrdpgyprdlmpppdla
                          138;
                         Indels
21.2%; Score 505; DB 21; 126.9%; Pred. No. 4.4e-37; ive 81; Mismatches 137;
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Job time: 63 sec
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                                                                                                                       vlqlvvdvdgn------
                         Matches 131; Conservative
              Similarity
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               Local
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2378
1 MKLANWYWLSSAVLATYGFL......GYKSSFKEAKMMIRPKHFKP 439
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                   195891 seqs, 67900655 residues
                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

195891

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_66:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	fibrinogen-like pr	cytotoxic I-lympho	fibrinogen-like pr		fibrinogen-related	fibrinogen gamma-B		fibrinogen beta ch	fibrinogen beta ch	fibrinogen gamma-B	fibrinogen beta ch	fibrinogen gamma c	ficolin-A precurso	fibrinogen alpha c	fibrinogen-related	ficolin-beta - piq	fibrinogen beta ch	transforming growt	fibrinogen gamma c	ficolin-1 precurso	restrictin precurs	janusin precursor,	fibrinogen gamma-A	fibrinogen gamma-B	О	tenascin-X - piq (tenascin-X - bovin	tenascin-X precurs	tenascin precursor
SUMMARIES	ID	137391	A27447	I56934	A38463	JN0596	FGHUGB	FGHUG	A25052	FGBOB	S05313	FGHUB	A32670	JC5980	D44234	A35084	B47172	A05299	A47172	FGLMGS	S61517	JH0675	A45445	FGRTGA	FGRTGB	S28170	S65944	T42629	A40701	JQ1322
	DB	7	7	7	7	7	Н	Н	7	Н	7	Н	7	7	~	7	7	7	7	Н	7	ď	7	Н	~	7	7	7		-
	Length	439	432	432	463	312	453	437	479	468	444	491	438	334	866	282	326	328	323	432	326	1353	1356	437	445	220	417	4135	9	2019
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Result	No.	1	7	3	4	2	9	7	œ	6	10	11	12	13	14	15	16	. 17	18	19	20	21	22	23	24	25	26	27	28	29

tenascin-X - mouse probable tenascin	tenascin-C - human tenascin precursor	tenascin precursor tenascin Y precurs	fibrinogen alpha-I scabrous locus (sc	scabrous protein p hypothetical prote	hypothetical prote hypothetical prote	microfibril-associ hypothetical prote	
148839 T09070	A32160 S19694	A32230 T42635	A41932 A39832	S58998 T15876	T21773	PC2036 T32255	T29850 T26827
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860 4006	174	181(64.	774 463	91:	12.	45
16.5 16.5	16.3	16.2 16.1	15.0 14.6	14.6 9.1	8 8 .3 .3	7.8	6.7
393.5 393.5	388	386 382.5	356.5	346.5	198 198	184.5 160	160 160
30	33 33	34 35	36	38 39	40	42	44

ALIGNMENTS

RESULT 1 137391 (fibrinogen-like protein expressed in T lymphocytes (pT49) - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Sate: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000 C; Accession: 137391; S47273 R; Ruegap, C:: Pytela, R. Gene 160, 257-262, 1995 A; Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib	A;Arcessiou: 19731 A;Betus: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1439 KRES. A;Residues: 1439 KRES. A;Costalues: Laya KRES. A;Costalues: Laya KRES. A;Orte: submitted to the EMBL Data Library, August 1994 C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology F;210-435/Domain: fibrinogen beta/gamma homology <fbg></fbg>	Query Match 100.0%; Score 2378; DB 2; Length 439; Best Local Similarity 100.0%; Pred. No. 2.8e-157; Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 MKLANMYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVS 60	61 LPPLTIQLPKOFSRIEEVFKEVQNLKEIVNSLKKSCODCKLOADDNGDPGRNGLLLPSTG 120 	1 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL 180 	1 TFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEV 240 	1 YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300 	1 RIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPD 360 	1 KDNDRYPSGNCGLYXSSGWWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGG 420
RESULT 137391 fibrinog C; Specie C; Date: C; Access R; Ruegg, Gene 160 A, Title:	A, Access A, Status A, Molecu A, Cross A, Note: C, Superf	Query Match Best Local Matches 43	Qy Db	Oy 6 Db 6	Qy 121 Db 121	Qy 181 Db 181	Oy 241 Db 241	Qy 301 Db 301	Qy 361 Db 361
			ŷ 1) I	J 11	ŷ	ŷ 1	J 1	J , L

PID:91042170

homology

4 ;

Gaps

7;

300 293 353 420

Tue Feb

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C;Species: Gallus gallus (chicken)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                        RIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 KDERAKDVCPVRLESRGKC----EEAGE-CPYQVSLPPLTIQLPKQFSRIEEVFKEVQN-
                                                                                                                                                                                                                                                 1 MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL
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                                                                                                                                                                     Length 432;
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                                                                                                                                                                                                             Indels
                       NID:91042169; PIDN: AAB34823.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M58514; NID:g211779; PIDN:AAA48770.1; C;Superfamily: fibrinogen beta Chain; fibrinogen beta/gamma PF:73-202/Domain: fibrinogen disulfide ring homology cFDR>F;212-460/Domain: fibrinogen beta/gamma homology cFBG>
                                                                                  n beta/gamma
<FBG>
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                                                                                                                                                                     2;
                                                                                                                                                                 Score 1849.5; DB 2;
Pred. No. 1.1e-120;
2; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Accession: A38463
R; Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, Biochemistry 30, 3294, 1991
A; Title: The beta chain of chicken fibrinogen contain A; Reference number: A38463; MUID:91182745
A; Accession: A38463
A; Status: preliminary
A; Molecule type: MRNA
A; Residues: 1-463 <WEI>
                                                             A,Gene: musfiblp
C,Superfamily: fibrinogen gamma chain; fibrinogen
F;203-428/Domain: fibrinogen beta/gamma homology <
                                                                                                                                                                                                           42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibrinogen beta chain - chicken (fragment)
                                                                                                                                                                   77.88;
77.48;
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                                                                                                                                                                 Query Match 77.8%
Best Local Similarity 77.4%
Matches 340; Conservative
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      <RES>
  A;Residues: 1-432 <R
A;Cross-references:
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Best Local S:
Matches 137
                                        C; Genetics:
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C;Species: Mus sp. (mouse)
C;Date: 26-7u1-1996 #sequence_revision 26-Ju1-1996 #text_change 03-Dec-1999
C;Accession: 156934
R;Parr, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G.
J. Virol. 69, 5033-5038, 1995
A;Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-induce
A;Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-induce
A;Ritle: Association of mouse fibrinogen-like protein with murine hepatitis virus-induce
A;Ritle: Association of mouse fibrinogen-like protein with murine hepatitis virus-induce
A;Reference number: 156934
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                                                                                                                                                                                                                                                                         strong homology
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                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387156
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F;203-428/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                           RESULT 2
A27447
cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse C; Species: Mus musculus (house mouse)
C; Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-6; Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-6; C; Accession: A27447
R; Koyama, T; Haalı, L.R.; Haser, W.G.; Tonegawa, S.; Saito, H. Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
A; Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a st A; Reference number: A27447; MUID: 87175527
A; Accession: A27447
A; Molecule type: mRNA
A; Residues: 1-432 < KOY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE-TAEDSRVQELESQVNKLSSELKNAKDQIQGLQGRLETLHLVNMNNIENYVDNKVANL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 YCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEMIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.9%; Score 1853.5; DB 2;
illarity 77.7%; Pred. No. 5.6e-121;
Conservative 42; Mismatches 49;
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421 YKSSFKEAKMMIRPKHFKP
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Best Local S
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; PID:g211780 homology; fibrinogen disu

16;

atypical thrombin cleavage

Tue Feb

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C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in A;Description: fibrinogen cagulation
A;Pathway: blood coagulation
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma chomology
C;Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-453/Product: fibrinogen gamma-B chain #status experimental <MPT>
F;176-415/Domain: fibrinogen beta/gamma homology <FBG>
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                                                                         셤
                           δ
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C:Date: 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: JN0596
C:Accession: JN0596
C:Accession: JN0596
C:Attle: Molecular cloning and initial characterization of a novel fibrinogen-related ge A;Title: Molecular cloning and initial characterization of a novel fibrinogen-related ge A;Accession: JN0596; MUID:93290661
A;Reference number: JN0596; MUID:93290661
A;Reference number: JN0596; MUID:93290661
A;References: GB:D1446; NID:9329314; PIDN:BAA03336.1; PID:g393315
A;Experimental source: liver
C;Superfamily: fibrinogen beta/gamma homology
F;1-17/Domain: signal sequence #status predicted <SIG>F;1-17/Domain: signal sequence #status predicted <SIG>F;80-305/Domain: fibrinogen beta/gamma homology <FBG>
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                                                                                                                                                                                                                                                                                          QARLDGSTNFTRTWQDYKAGFGNLRR------EFWLGNDKIHLLTKSKEMILRID 303
                                                                                                                                                                                                                                                                                                                                                                                             LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALR--FNKHYN------HDLK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FFTTPDKDNDRY----PSGNCGLYYSSGWWFDACLSANLNGKYY-----HQKYRGVRN 403
---LKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELE 134
                                                                                                SEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSLDGKCSKC 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 GKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 -----LGSKRQ-------YADCSEIFNDGYKLSGFYKIKPLQSPAEFSVYCDMSD-G 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 GGWTVLQARLDGSTNFTRTWQDYKAGFGNL---RREFWLGNDKIHLLTKSKEMILRIDLE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKH-----YNHDLKFFTTP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                            108 VAKFSDTSTTMYQYVNMIDNKLVKTQKQRKD-----NDIILSEYNTEMELHYNYIK--D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 QVRLLETRVKQQQVKIKQLLQE-----NEVQFLDKGDEDTVVD------
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36.8%; Pred. No. 6.8e-28;
iive 38; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibrinogen-related protein HFREP-1 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 GIFWGTWPGVSEAHPGGYKSSFKEAKMMIRP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              437 GIVWMNWKG-----SWY--SMKKMSMKIKP 459
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Best Local Similarity 36.8%
Matches 118; Conservative
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A **Recision: A**Pata **

A **Residues: 286-453 < FORD*

A **Residues: 286-453 < FORD*

B **Recision: A**Pata **

A **Recision: A**Pata **

A **Recision: A**Pata **

A **Recision: A**Pata **

A ***Recision: A**Pata
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-113, 1', 115-453 <RIX>
A; Cross-incering type: DNA
A; Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:9182438; PIDN:AAB
A; Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A; Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near t
A; Reference number: A92448; MUID:85030379
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A;Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
A;Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
A;Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
A;Introns: 26/3; 41/3; 103/1; 134/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/2; 17/
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419 GGYKSSFKEAKMMIRPKHFKP 439
                                                                                                A; Gene: GDB: FGG
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H., and

gamma fibrinogen chains:

near

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A; Molecule type: protein
A; Residues: 27-33, XX, 36-41 < BER>
A; Experimental source: thrombin-activated platelets
A; Note: sequence extracted from NCBI backbone (NCBIP:133734)
R; Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Bjochemistry 33, 1984-1993, 1994
A; Title: Identification of proteins associated with apolipoprotein A-I-containing lip
A; Reference number: A54223; MUID:94162201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X00086; NID:g31445; PIDN:CAA24944.1; PID:g577055
R;Bertagnolli, M.E.; Beckerle, M.C.
J. Cell Biol. 121, 1329-1342, 1993
A;Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with A;Reference number: A40698; MUID:93286185
A;Accession: A40698
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 276-437 <KAN>
K; R; Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
K; Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A; Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing
A; Reference number: A92448; MUID:85030379
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                                                                                                                                                             A;Molecule type: protein
A;Residues: 27-437 (HEN>
R;Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A;Title: Partial mRNA sequences for human Aalpha, Bbeta, and A;Reference number: A93956; MUID:83247396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: DNA
A; Residues: 286-437 < FOR>
R; Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries,
Nucleic Acids Res. 11, 7427-7434, 1983
A; Fitle: Isolation and characterisation of cDNA clones for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: 137393; MUID:84069777
A; Accession: 137393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 209-270 <RES>
                                                                                                                                       A; Accession: C94433
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                                           an
                                           the alpha chain of
F;341-355/Domain: calcium binding #status predicted <CAB>
F;400-422/Region: polymerization site, binding to the amino end of the alpha chain e:34/Disulfide bonds: interchain (to gamma-35) #status predicted
F;35/Disulfide bonds: interchain (to gamma-35) #status predicted
F;45/Disulfide bonds: interchain (to beta-110) #status predicted
F;45/Disulfide bonds: interchain (to alpha-64) #status predicted
F;78/Binding site: carbohydrate (Asn) (covalent, #status predicted
F;78/Binding site: carbohydrate (Asn) (covalent, #status predicted
F;161/Disulfide bonds: interchain (to beta-227) #status predicted
F;165/Disulfide bonds: interchain (to alpha-180) #status predicted
F;179-208,322-365/Disulfide bonds: #status predicted
F;44/Cross-link: isopeptide (Lys) (interchain to gamma-424-Gln) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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VELEDWNGRTSTADYAMFKVGPEADKYRLTYAYFAGGDAGDAFDGFDFGDDPSDKFFTSH 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 LKSRKMLEEIMKYEASILTHDSSIRYLQ-----EIYNSNN-----QKIVNLKEKVAQL 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TCGIADFLSTYQTK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVSLPPLTIQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDKDLQSLEDILHQVENKTSEVKQLIKAIQ-LTYNPDESSKPNMI------DAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIWATWKTRWYSMKKTTMKIIPFNRLTIGEGOQHHLGGAK------QVRPEH 438
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 453;
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                                                                                                                                                                                                                                                                                                                                                                                                                            20.4%; Score 484.5; DB 1;
29.7%; Pred. No. 3.8e-26;
live 56; Mismatches 178;
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Best Local Simi
Matches 141;
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cDNA clones for the Aalpha- and gamma-chai

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fibrinogen gamma-A chain precursor - human
N;Alternate names: coagulation factor I
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 25-Feb-1985 #text_change 21-Jul-2000
C;Accession: A90470; B90494; C94433; B93956; B92448; I37393; A40698; H54223; A03125; C37
R;Chung, D.W.; Chan, W.Y.; Davie, E.W.
B;Chung, D.W.; Chan, W.Y.; Davie, E.W.
B;Chemistry 22, 3250-3256, 1983
A;Title: Characterization of a complementary deoxyribonucleic acid coding for the gamma
A;Reference number: A90470; MUID:83283434
A;Ressious: 1-437 <CHU>
R;Rixon, M.W.; Chung, D.W.; Davie, E.W.
B;Acochemistry 24, 2077-2086, 1985
A;Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A;Reference number: A90494; MUID:85252774
A;Accession: B90494
A;Residues: 1-113,'I',115-437 <RIX>
A;Residues: 1-113,'I',115-437 <RIX>
A;Cross*:references: GB:X02415; GB:M10014; NID:g182438; PIDN:AAB59531.1; PID:g182439
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A; Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bond A;Reference number: A90041; MUID:84305751 A;Contents: annotation; review, EM structure, polymerization, ligands R;Horwitz, B.H.; Varadi, A.; Scheraga, H.A. A;Reference number: A94437
A;Contents: annotation; disulfide bonds
R;Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A;Reference number: A94309; MUID:76225080
A;Reference number: anotation; disulfide bonds A; Contents: annotation; quaternary structure, disulfide bonds A; Reference number: A90467; MUID:83231465 Annu. Rev. Biochem. 53, 195-229, 1984 A;Title: Fibrinogen and fibrin. R; Hoeprich, P.D.; Doolittle, R.F. Biochemistry 22, 2049-2055, 1983 R; Doolittle, R.F

R;Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G. in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., F. A;Title: The structures of fibrinogen and fibrin.

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AZJOLA
AZ
                           -DAAT 109
                                                                                                                                                                       334 NGMQFSTWDNDNDKF-EGNCAEQDGSGWWMNKCHAGHLNGVYYQGGTYSKASTPNGYDNG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 IDLEDFNGVELYALYDQFYVANEFLKYRLHVGNY-NGTAGDAL-RFNKHYNHDLKFFT-- 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 VELEDWNGRTSTADYAMFKVGPEADKYRLTYAYFAGGDAGDAFDGFDFGDDPSDKFFTSH 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- OKYRGVRNG 404
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                                                                                                                                                                                                                                                                                                                                              DGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETM
                                                                                                            NRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGWTVLQARLDGSTNFTRTWQDYKAGFGNL - - - - RREFWLGNDKIHLLTKSKEM - ILR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYH----
                      62 VDKDLQSLEDILHQVENKTSEVKQLIKAIQ-LTYNPDESSKPNMI·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.2%; Score 479.5; DB 2; 29.2%; Pred. No. 9e-26; ive 66; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --YKISMLK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                         A KRETERICE number: A 204843; MILL: 8420423; MILL: 8420481; MALL: MAUL: 8420481; MILL: 8420481; A.H.: Meyer, D.; Marguerie, G.; Ginsberg, M.H.

7. Blol. Chem. 259, 5388-5391, 1984
A; Title: Evidence that three adhesive proteins interact with a common recognition site of A; Reference number: A92477; MUID: 84185664
A; Title: Evidence that three adhesive proteins interact with a common recognition site of A; Reference number: A92477; MUID: 84185664
A; Title: Evolatization of a fibrinogen calcium binding site between gamma-subunit positic A; Reference number: A92549; MUID: 85561382
A; Contents: annotation; calcium binding region
R; Riizschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A; Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-te A; Reference number: A37117; MUID: 9337977
A; Contents: annotation; homentin cleavage site
A; Note: hementin, a protease from Haementeria ghilianii, the giant South American leech, C; Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili ger) and between alpha chains are synthesized in the liver.
C; Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili ger) and between alpha chains are synthesized in the liver.
C; Comment: The two forms of gamma chain, and B (see PIR:FGHUGB), arise by alternate spintron, which makes this chain different from the gamma-B chain at positions 434-437 and converted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:119132; OMIM:134850
A; Map position: 4q28-4q28
A; Map position: 4q28-4q28
A; Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
C; Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG ins are contained in the core. Two three-chain coiled coils emerge from this core and cfrom the distal domain nodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A peachpetion: fibrinogen cleaved by thrombin yields monomers that are polymerized into A pathway: blood coagulation
A pathway: blood coagulation
C Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C Styvords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein;
E;1-26/Domain: signal sequence #status predicted <SIG>
E;1-26/Domain: signal sequence #status predicted <SIG>
E;1-25/Domain: fibrinogen gamma homology <FBG>
E;1-25/Domain: fibrinogen beta/gamma homology <FBG>
E;1-25/Domain: calcium binding #status predicted <CAB>
E;1-25/Domain: calcium binding #status sexperimental
E;1-25/Disulfide bonds: interchain (to gamma-35) #status experimental
E;1-25/Disulfide bonds: interchain (to alpha-64) #status experimental
E;1-25/Disulfide bonds: interchain (to alpha-64) #status experimental
                                                                                                                                                                                    R;Kloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.
Bochbenistry 23, 1767-174, 1984
A;Title: Platelet receptor recognition site on human fibrinogen. Synthesis and structure A;Reference number: A90483; MUID:84203545
Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984
A;Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374
A;Reference number: A94006; MUID:85014892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TCGIADFLSTYQTK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Contents: annotation; polymerization region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: GDB: FGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
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LPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGD 127

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fibrinogen gamma-B châin precursor - bovine ('Species: Bos primigenius taurus (cattle) ('Species: Bos primigenius taurus (cattle) ('Species: Bos primigenius taurus (cattle) ('Sacession: S05313 R. Sequence_revision 07-Sep-1990 #text_change 13-Aug-1999 ('Sacession: S05313 R. Secondary R. M.; Poreman, R.C.; Saunders, N.R. Nuclecies Res. 17, 6397, 1989 A; Title: Nuclecide and deduced amino acid sequence of a gamma subunit of bovine fibr A; Reference number: S05313; MUID:89366676
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A;Cross-references: EMBL:X15556; NID:g349; PIDN:CAA33562.1; PID:g350
A;Note: the authors translated the codon AGT for residue 105 as Ala and ATT
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>
F;174-414/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 MYLIQPEDSSKPYRVYCDMKTEKGGWTVIQNRQDGSLDFGRKWDPYKQGFGNIATNAEGK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----EFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 NYNGTAGDAL-----RFNKHYN-HDLKFFTTPDKDNDRY----PSGNCGLYYSSGWW 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 FDACLSANLNGKYY-----HQKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIR 433
                                                                                                                                                                                                                                                                                                                                                         LPPLTIQLPKQFSRIEE-VFKEVQNLKEIVNSLKKSCQDC---KLQADDNGDPGRNGLLLP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----QNQVQDNENVVNEYSS------HLEKHQLYIDETVKNNIPTKL 172
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                                                                                                                                                                                                                                                                                                                                                                                                   LCPTGCKLQDTLVRQERPIRKSIEDLRNTVDSVSRTSSSTFQYITLLKNMWKGR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 ANLTFVVNSLDGKCSKCPSQEQIOSR-----PVQHLIYKDCSDYYAIGKRSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 TYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRR----
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F;215-464/Domain: fibrinogen beta/gamma homology <FBG>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experim
F;6/Modified site: sulfate (Tyr) (covalent) #status experimental
F;21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F;31/Rhinding site: carbohydrate (Asn) (covalent) #status predicted
F;372-373/Cleavage site: Arg-Thr (plasmin) #status experimental
                                                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                      ; Score 470; DB 1; Length 46; Pred. No. 4e-25; 57; Mismatches 149; Indels
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30.6%;
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A; Residues: '1-444 <BRO>
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Best Local Simi
Matches 142;
                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 129;
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                                                                  218 CTVNCRVPVVSGMHCEDIYRNGGRTSEAYYIQPDLFSEPYKVFCDMESHGGGWTVVQNRV 277
                                                                                                                                                                                                                                                                 DGSTNFTRWQDYKAGFGNLR------REFWLGNDKIHLLTKSKEMILRIDLEDF 307
                                                                                                                                                                                                                                                                                                                                                                                    NGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDAL-----RFNKHYN-HDLKFFTT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDKDNDRY----PSGNCGLYYSSGWWFDACLSANLNGKYY-----HQKYRGVRNGIFW 407
                                                                                                                                                 -----VQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARL
                           EEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSLDGKCSK----CPSQEQIQSRP
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A; Paterence number: A94437
A; Contents: annotation; disulfide bonds
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Ccomment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stab ger) and between alpha chains (weaker) of different monomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ins are contained in the core. Two three-chain coiled coils emerge from this core and from the distal domain nodes.
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C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
C:Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglutamic
F;1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>
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C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see
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Ann. N. Y. Acad. Sci. 408, 449-456, 1983
A;Title: Cloning of fibrinogen genes and their cDNA.
A;Reference number: 949038; MUID:83254384
A;Contents: annotation
R;Watt, K.W.K.; Takagi, T.; Doolittle, R.F.
Biochemistry 18, 68-76, 1979
A;Title: Amino acid sequence of the beta chain of human fibrinogen.
A;Reference number: A90437; WUID:79124640
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A; Contents: annotation; disulfide bonds
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Annu. Rev. Biochem. 53, 195-229, 1984
A;Title: Fibrinogen and fibrin.
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J. Biol. Chem. 265, 13669-13676, 1990
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N.Alternate names: coagulation factor I
N.Cortains: 1fbrinogen Resequence revision 31-Mar-1993 #text_change 22-Jun-1999
C.Accession: B43568, A80469; B90469; I37389; A94433; A90437; A94309; G5422; A03121; B37
Adv. Exp. Med. Biol. 281, 39-48, 1999
C.Accession: B43568 wIDL: 281, 39-48, 1999
A.Accession: B43568 wIDL: 91344740
A.Accession: B43568 wIDL: 91344740
A.Michecule type: DNA
A.Michecu
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                                                  69 PKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN 128
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                                                                                                                                                                                                                                               RVRELESEVNKLSSELKNAK---EEINVLHGRLEKLNLVN------MNNIENYVDSKV 177
                                                                                                                                                                                                                                                                                                                                          ----PSKPNNIESATKNSKSMMEEI-----MKYETLISTHESTIRFLQEVYNSNSQKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                178 ANLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSS
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                                                                                                                                                   DKDLRTLEGILYQVENKTSEARELVKA----IQISYNPDQ---
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Best Local Similarity 30.4%;
Matches 130; Conservative (
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                      A: Status: preliminary;
A: Molecule type: mRNA
A; Residues: 1-58 < BHA>
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                                                                  F.45-47/Region: polymerization site
F.99-228/Domain: fibrinogen disulfide ring homology <FDR>
F.218-48/Tobmain: fibrinogen beta-gamma homology <FDR>
F.218-48/Tobmain: fibrinogen beta-gamma homology <FDR>
F.31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiments
F.34-45/Cleavage site: Arg-Gly (thrombin) #status experimental
F.35/Disulfide bonds: interchain (to alpha-55) #status experimental
F.30/Disulfide bonds: interchain (to alpha-68) #status experimental
F.227/Disulfide bonds: interchain (to alpha-68) #status experimental
F.227/Disulfide bonds: interchain (to alpha-184) #status experimental
F.227/Disulfide bonds: interchain (to gamma-45) #status experimental
F.237-31:316.241-270.424-437/Disulfide bonds: #status experimental
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R:Rbhattacharya, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J.
Woll. Cell. Endocrinol. 72, 213-220, 1990
A;Title: Isolation and characterization of CDNA clones for the gamma subunit of Xenopus A;Reference number: I51416; MUID:91146806
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fibrinogen gamma chain - African clawed frog
Cispecies: Xenopus laevis (African clawed frog)
Cispecies: Xenopus laevis (African clawed frog)
Cispecies: Xenopus laevis (African clawed frog)
Cispecies: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 13-Aug-1999
Cispecies: X32670; I51416
Ripastori, R.L.; Moskaitis, J.E.; Smith Jr., L.H.; Schoenberg, D.R.
Biochemistry 29, 2599-2605, 1990
A:Reference number: A32670; MUID:90241882
A:Accession: A32670
A:Status: preliminary
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-438 <-PAS>
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                                                                                                                                                                                                                                                                                                                                                  F;394/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                         19.4%; Score 461; DB 1; Length 491; 28.7%; Pred. No. 1.8e-24; ive 57; Mismatches 161; Indels 112;
F;31-491/Product: fibrinogen beta cháin #status experimental <MAT>F;31-44/Product: fibrinopeptide B #status experimental <APT>F;45-491/Product: fibrin beta chain #status experimental <FGB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTWDMAKHGTDDGVVWMNWKG----SWY--SMKMSMKIRP 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.48
Best Local Similarity 28.73
Matches 133; Conservative
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A; Residues: 1-334 <FUJ>
A; Cross-references: DDBJ:AB007813; NID:92957011; PIDN:BAA25126.1; PID:d1026054; PID:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y.; Yagasaki, K.; Tachikawa,
                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 06-May-1998 #sequence_revision 29-May-1998 #text_change 18-Feb-2000
C;Accession: JC5980
R;Fujimori, Y.; Harumiya, S.; Fukumoto, Y.; Miura, Y.; Yagasaki, K.; Tachika Biochem. Biophys. Res. Commun. 244, 796-800, 1998
A;Title: Molecular cloning and characterization of mouse ficolin-A. A;Reference number: JC5980; MUID:98205801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 DGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 DLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYH------QKYRGVRN 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 KQFSRIEE-VFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN 128
                                                                                                                                                                                                                                                                  Gaps
A;Cross-references: GB:M35548; NID:g214141; PIDN:AAA03247.1; PID:g214142 C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology C;Keywords: blood coagulation F;173-413/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 RVRELESEVNKLSSELKNAKE-EINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 GSAWIVIQRRLDGSVNFHKNWVQYREGFGYLSPNDKTEFWLGNEKIHLLSTQSTIPYVMR
                                                                                                                                                                                                                                                                                                                             10 SSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVSLPPLTIQLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 GGGWTVLQARLDGSTNFTRTWQDYKAGFG----NLRREFWLGNDKIHLLTKSKEM--ILR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 IDLEDFNGVELYALYDQFYVANEFLKYRLHVGNY-NGTAGDAL------RFNKHY-NH
                                                                                                                                                                                                                                                               70;
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                                                                                                                                                                                                DB 2; Length 438;
                                                                                                                                                                                                ; Score 456; DB 2; Length 436; Pred. No. 3.4e-24; 69; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <COL>
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F;1-21/Domain: signal sequence #status predicted <SIG>
F;50-64,68-106/Domain: collagen-like #status predicted
F;123-334/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.0%; Score 452; DB 2; L 34.4%; Pred. No. 4.4e-24; tive 35; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                         14 SLALLSSAFGNIIPNTDNCCILDGRFGEYCPT------
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12;

Gaps

16;

Indels

us-09-442-143-2.rpr

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F:591-593/Region: cell attachment (R-G-D) motif
F:629-863/Domain: fibrinogen beta/gamma homology <FBG>
F:629-863/Domain: fibrinogen beta/gamma homology <FBG>
F:629-863/Domain: fibrinogen beta/gamma homology <FBG>
F:22,460/Binding site: phosphate (Ser) (covalent) #status experimental
F:35-78 sulfide bonds: interchain (to alpha-47) #status experimental
F:64/Disulfide bonds: interchain (to gamma-49) #status experimental
F:68/Disulfide bonds: interchain (to beta-95) #status experimental
F:68/Disulfide bonds: interchain (to beta-106) #status experimental
F:180/Disulfide bonds: interchain (to beta-223) #status experimental
F:180/Disulfide bonds: interchain (to beta-223) #status experimental
F:322/Cross-link: isopeptide (Lys) (interchain to alpha-2-plasmin inhibitor 41-Gln) #
F:347,385/Cross-link: isopeptide (Lys) (interchain to alpha) #status experimental
F:461-491/Disulfide bonds: #status experimental
F:527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to alpha) #status pred
F:66,831/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 KEVQNLKEIVNSLKKSCQDCKLQADDNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 32.5% Matches 136; Conservative
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Matches 99; Conservative
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A; Residues: 1-282 <XUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A35084
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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C.Species: Howo saplens (man)
C.Accession: 10-4013/31 sequence_revision 06-Sep-1996 #text_change 02-Sep-2000
C.Accession: 10-4023/31 sequence_revision 06-Sep-1996 #text_change 02-Sep-2000
C.Accession: 10-4023/31 sequence_revision 10-4023/31 sequence_revision.
B.Accession: 10-4023/4 MUID: 91090725
B.Actrus: translated from GG/EMBL/DDBJ
A.Residues: 1-866 cFU13
A.Residues: GENERS (MID: 9102406; PID: 9182407
A.Rote: neither the complete nucleic acid sequence nor the complete translation are show.
A.Rote: neither the complete nucleic acid sequence nor the complete translation are show.
A.Rote: neither the complete nucleic acid sequence nor the complete translation are show.
A.Rote: neither the complete nucleic acid sequence nor the complete translation are show.
A.Rote: neither the complete nucleic acid sequence nor the complete translation are show.
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A.Rote: neither the complete nucleic acid sequence nor the complete translation are show.
A.Rote: sequence extracted from NCBI backbone (NCBIP:11)9917
A.Rote: sequence extracted from NCBI backbone (NCBIP:11)9917
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A.Rote: sequence extracted from NCBI backbone of the soft lot.
C.Comment: The soft not of the formation of the soft lot.
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C.Comment: Sledic Scoper acid sequence of the list of not nois sequence acid lot.
A.Rote: the list of not nois is incomplete
C.Comment: Sledic Scoper acid on search and connect it to fluction:
A.Rote: the list of not nois is incomplete
C.Comment: Sledic Scoper Sc
      107 GDPGRNGLLLP--STGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLV 164
                                                                                                                                                                                                   ----RSCKDLLTRGIFLT 137
                                                                                                                                                                                                                                                                                                                              GWYTIHLPDCR--PLTVLCDMDVDGGGWTVFQRRVDGSIDFFRDWDSYKRGFGNLGTEFW 195
                                                                                                                                                                                                                                                                                                                                                                                                LGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNY-NGTAGDA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                    LRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR 402
                                                                                                                                       NMNN1 ENYVDSKVANLTFVVNSLDGKCSKCPSQEQ1QSRPVQHL1YKDCSDYYA1GKRSS
                                                                                                                                                                                                                                                               ETYRV-TPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extended splice form - human
                                                                     74 GSPGKMG---PAGSKGEPGTMGPPGVKGEKGDTGAAPS---LGEKELG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| ||| |||
DGINWGTGQ------GHHYSYKVAEMKIR 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGIFWGTWPGVSEAHPGGYKSSFKEAKMMIR 433
                                                                                                                                                                                                ----DTLCORGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: coaquiation factor
N;Contains: fibrinopeptide A
C;Species: Homo sapiens (man)
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fibrinogen-related protein A precursor - sea cucumber (Parastichopus parvimensis)
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Proc. Natl. Acad. Sci. U.S.A. 87, 2097-2101, 1990
A;Title: Presence of a vertebrate fibrinogen-like sequence in an echinoderm.
A;Reference number: A35084; MUID:90192754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Parastichopus parvimensis
C;Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 09-Sep-1997
C;Accession: A35084
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                      118 STGAP--GEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLE-------KLN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----RREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  700 NDEGEGEFWLGNDYLHLLTQ-RGSVLRVELEDWAGNEAYAEY-HFRVGSEAEGYALQVSS 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 YNGTAGDAL-----RFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           758 YEGTAGDALIEGSVEEGAEYTSHNNMQ -- - FSTFDRDADQWEE - NCAEVYGGGWWYNNCQ 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                              163 LVNMNNIENYVDSKVANLTFVVNS-LDGKCSKCPSQEQIQSRPVQHLIYKDCSDY---YA
                                                                                                                                                               586 STSYNRGDSTFESKSYKMADEAGSEADHEGTHSTKRGHAKSRPV-----RDCDDVLQTHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 IGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 SANLNGKYY------HQKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||||| || : : | : || : |||| AANLNGIYYPGGSYDPRNNSPYE-IENGVVWVSFRGAD------YSLRAVRMKIRP
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Length 866;
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                                                                Indels
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C;Superfamily: fibrinogen beta/gamma homology
F;67-280/Domain: fibrinogen beta/gamma homology <FBG>
                                                          51; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.8%; Score 446; DB 2; 43.2%; Pred. No. 9.2e-24; tive 33; Mismatches 75;
19.0%; Score 451; DB 2; 32.5%; Pred. No. 1.9e-23;
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Search completed: February 27, 2001, 12:50:10 Job time: 154 sec

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COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THEN PC COMPATION:
COMPUTER: THEN PC COMPATION:
COMPUTER: THEN PC COMPATION:
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING NOWAER: US/08/525,505A
FILING DATE: 22-SEP-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/JP94/00455
FILING DATE: 22-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00455
FILING DATE: 23-MAR-1993
ATYONEY/AGENT INFORMATION:
NAME: OBLOW, NOWAER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION INFORMATION:
TELEPRAK: 703-413-3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
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MOLECULE TYPE: protein

US-08-525-505A-2
                                                                                     (without alignments)
374.141 Million cell updates/sec
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1 MKLANWYWLSSAVLATYGFL......GYKSSFKEAKMMIRPKHFKP 439
                                                                      February 27, 2001, 12:47:34; Search time 21.07 Seconds
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Sequence 1
Sequence 4
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                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-162-437-6

US-08-960-507-20

US-08-525-505A-4

US-08-93-821-4

US-08-960-507-4

US-08-960-507-19
                                                                                                                                                                                                                                  hits satisfying chosen parameters:
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US-08-348-492-4
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US-08-960-507-2
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US-08-348-492-2
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                                                                                                                                                                                                           174772 seqs, 17957048 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                        Listing first 45 summaries
                                                protein search, using sw model
                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUST ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 STATE: VA

USA

COUNTRY:

22202

LENGTH: 314 amino acids TYPE: amino acid SEQUENCE CHARACTERISTICS:

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APPLICANT: YOSHIMURA, HIROMITSU
APPLICANT: MATSUKI, YUMIKO
APPLICANT: SHINDO, SAEKO
APPLICANT: HANADA, KAZUNORI
TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
WUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                               US-00-812-586-49
US-08-960-507-21
US-09-167-647-2
US-09-13-812-6
US-08-933-821-6
US-08-960-507-6
US-08-167-647-1
US-08-167-647-1
US-09-167-647-1
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-08-404-781-4
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                                                                     125 VGD-NRVRE---LESEVNKLSSELKNAKEEI-NVLHGRLEKLNLVNMNNIENYVDSKVAN 179
                                                                                                                                          180 LIFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFE 239
                                                                                                                                                            240 VYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNL---RREFWLGNDKIHLLTKSK 296
                                                                                                                                                                                                                                     409
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                          23 LGDENCLQEQVRLRAQVRQLETRVKQQQVVIAQLLHEK--EVQFLDRGQEDSFID---- 75
                                                                                                                                                                                                                                                                                    297 EMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKH-----YN
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DYTLKIDLTDFEKNSRFAQYEKFKVGDEKSFYELNIGEYSGTAGDSLSGTFHPEVQWWAS
                                                                                                                                                                                                                                                                                                                                                       351 HDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRG-VRNGIFWGT
                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
TITLE OF INVENTION: THEREOF
TUMBER OF SEQUIENCES: 6
CORRESPONDENCE ADDRESS:
   Length 314;
                                      46; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
   Score 524; DB 1;
Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                            410 WPGVSEAHPGGYKSSFKEAKMMIRPKHFKP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,579
FILING DATE: 17-JAN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,503
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
FILING DATE: 02-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08373579
Patent No. 5650490
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : (914) 345-7400
(914) 345-7721
 22.0%;
37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Query Match , 22.0
Best Local Similarity 37.6
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 777 01d
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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US-08-373-579-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                                                                                                                                                                                                                                                                      85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 IMENNTOWLMKLENYIQDNMKKEMVEIQQNAVQN------QTAVMIEIGTNLLNQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----NKLSSELKNAKEEINVLHGR---LEKL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 TAEOTRKLTDVEAQVLNQTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NMNNIENYVDSKVANLTF------V 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254
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                                                                                                                                                                                                                                                                                                            43 LESRGKCE---EAGECPYQVSLPPL------TIQ--LPKQFSRIEEVFKEVQN 84
                                                                                                                                                                                                                                                                                                                                                     26 MDSIGKKOYOVOHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD
                                                                                                                                                                                                                                                            74; Mismatches 159; Indels 124;
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                                                                                                                                                                                                                Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DAVIS, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND TITLE OF INVENTION: THEREOF
NUMBER OF SOUGENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                              22.0%; Score 522; DB 1; 27.9%; Pred. No. 5.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Regeneron Pharmaceuticals, Inc. 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08418595
Patent No. 5814464
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                              Matches 138; Conservative
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 SSFKEAKMMIRPKHF 437
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                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-373-579-6
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MEDIUM TYPE: Floppy
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Best Local Similarity
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STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10591
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FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-2113
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 27.99
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 496 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-665-926-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                           Tarrytown
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      RESULT 4
US-08-665-926-6
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Best Local Similarity 27.9%; Pred. No. 5.9e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 IMENNTQWLMKLENYIQDNMKKEMVEIQQNAVQN-------QTAVMIEIGTNLLNQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 -----RVRELESEV----LEKL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 TAEQTRKLTDVEAQVLNQTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
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REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEPHONE: (914) 345-7721
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
                                                                                                                                                                                                       PRIOR APPLICATION DETA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SLKATTMMIRPADF 496
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; MOLECULE TYPE: protein
US-08-418-595-6
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Best Local Similarity
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85 LKE-----IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
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                                                                                                                                                                                          APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STALL.
COUNTRY: U.S.A.
ZIP: 10591-6707
ZIP: 10591-6707
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPAtible
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
ADTEMPTION PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: REG 330-H
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-UUN-1996
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Sequence 6, Application US/08665926; Patent No. 5851797; GENERAL INFORMATION:
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364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                                                                                                                                                                                                               184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD 243
                                                                                                                                                                                                                                                                                                                                                                           ||:| | : ::||:: :||355 VINILITMMSTSNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTFPNSTEEIKAYCD 314
                                                                                                                                                                                                                                                                                                                                                                                                                                            244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLITKSKEMILRID 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 DKCIC-KCSQMLTGGWWFDACGPSNLNGMYYPQRQNTNKFNGIKWYYWKG-----SGY- 482
                                                  ---IVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDN---- 128
                                                                                               86 IMENNTQWLMKLENYIQDNMKKEMVEIQQNAVQN------QTAVMIEIGTNLLNQ 134
                                                                                                                                                 -----NKLSSELKNAKEEINVLHGR---LEKL 161
                                                                                                                                                                                              135 TAEQTRKLTDVEAQVLNQTTRLELQLLEHSLSTNKLEKQILDQTSEINKLQDKNSFLEKK 194
                                                                                                                                                                                                                                                                                             195 VLAMEDKHIIQLQSIKEEKDQLQVLVSKQNSIIEELEKKIVTATVNNSVLQKQQHDLMET 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 MDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLEN 85
                                                                                                                                                                                                                                                ---NMNNIENYVDSKVANLTF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC*DOS/MS-DOS
SOCFWARE: Winparin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/08960507
Patent No. 6057435
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands:
WUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P1
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California
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                 129 ----RVRELESEV----
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COMPUTER READABLE FORM:
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                                                  85 LKE----
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                              364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.0%; Score 522; DB 3; Length 496; Best Local Similarity 27.9%; Pred. No. 5.9e-40; Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps
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                                                                                                                                                                                                                                                            Sequence 6, Application US/09162437
Patent No. 6166185
GENERAL INFORMATION: et al.
APPLICANT: Davis, et al.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/162,437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION DATE: 06-APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
TING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
FILING PAPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILLING MANAGE CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/418,595
FIFTING DATE: 06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cobert, Robert J. REGISTRATION NUMBER: 36,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: RI
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TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 6:
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483 -SLKATTMMIRPADF 496
                                                                                            423 SSFKEAKMMIRPKHF 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-162-437-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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US-09-162-437-6
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33,055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genertech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,(
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 650/225-3216
650/952-9881
                                          : 312 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 26.9
Matches 131; Conservative
                   SEQUENCE CHARACTERISTICS
                                                                                                    ; MOLECULE TYPE: protein US-08-525-505A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                     linear
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                                                                                   TOPOLOGY:
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US-08-933-821-4
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                                        LENGTH:
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                                                                                                                                                                                                                                                                                                              225 C-KCSQMLTGGWWFDACGPSNLNGMYYPQRQNTNKFNGIKWYYWKG-----SGY--SLK 275
                                                                                                                                                                                                        188 DGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETM 247
                                                                                                                                                                                                                                                                                    248 GGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDF 307
                                                                                                                                                                                                                                                                                                                                                                     308 NGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYP 367
                                                                                                                                                                                                                                                                                                                                                                                             SGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVR-NGIFWGTWPGVSEAHPGGYKSSFK 426
                                                                                                                     NRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSL 187
                                                                                                                                                4 DQLQVLVSKQNSIIEELEKKIVTATVNNSVLQKQQHDLMETVNNL-----LTMMSTSN 56
                                                                              29;
                                    Length 286;
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Patent No. 580711
GENERAL INFORMATION:
APPLICANT: HARA, HIROSHI
APPLICANT: MATGUKI, YUMIKO
APPLICANT: SHINDO, SAEKO
APPLICANT: HANADA, KAZUNORI
TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                              49; Mismatches 121; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUS:
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : PatentIn Release #1.0, Version #1.30
                                      DB 3;
                                    Score 506.5; DB 3 Pred. No. 6.9e-39;
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APPLICATION NUMBER: PCT/JP94/00455
FILING DATE: 22-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-063905
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,505A
FILING DATE: 22-5EP-1995
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-220
TELEFAX: 703-413-2220
                                      21.3%;
                                                                            Conservative
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REGISTRATION NUMBER: 2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 ATTMMIRPADF 286
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                                                           Best Local Similarity
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                                                                              Matches 112;
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                                      Query Match
                                                                                                                                                                                                                                                                                                                             109
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                                                                                                                       270 DYKAGFGNL---RREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFL 326
                                                                                                                                                                                                                                                                               327 KYRLHVGNYNGTAGDALRFNKH----YNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWW 380
                                                                                                                                                                                                                                                                                                         381 FDACLSANLNGKYYHQKYRG-VRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHFKP 439
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                          210 YKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQ
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26.9%; Pred. No. 2.2e-3%;
ive 81; Mismatches 137; Indels 138;
    Length 312;
                                                  Indels
21.3%; Score 506; DB 1;
44.6%; Pred. No. 8.8e-39;
tive 25; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPUTEDS
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/933,821
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US-08-933-821-4
; Sequence 4, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
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                                                                                                   ----IVNEVKLLRKESRNMNSRVTQLYMQ 136
                                                                                                                                    158 L-----EKLNLVNMNNIENYV-----L-DSKVANLTFVVNS-----L 187
                                                                                                                                                                                                                                      197 EEQCLRIFSRQDTHVSPPLVQVVPQHIPNSQQYTPGLLGGNEIQRDPGYPRDLMPPPDLA 256
                                                                                                                                                                                                                                                                                                      257 ISPIKSPFKIPPVIFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDPG 316
                                                                                                                                                                                                                                                                                                                                         GWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNG 309
                                                                                                                                                                                                                                                                                                                                                          310 VELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTFPDKDNDRYPSG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                            430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCGLYYSSGWWFDACLSANLNGKYYH-QKYRGV-RNGIFWGTWPGVSEAHPGGYKSSFKE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKCEEAGECPYQVSLPPLTIQLP-----KQFSRIEEVF--KEVQNLKEIVNSLKKSCQ
                                                                                                                                                                                                                                                                         -----IYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGG
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   188 DGKCSKCPSQEQIQSRP-----VQHL-----
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APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08960507 Patent No. 6057435
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CITY: South San Francisco
STATE: California
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ATTORNEY/AGENT INFORMATION:
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                                                                                                   101 VLQLVVDVDGN-----
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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431 NCAHFHKGGWWYNACAHSNINGVWYRGGHYRSKHQDGIFWAEYRG-----GSY--SLRA 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 VELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSG 369
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                                                                                                                                                                                                                                                                                            42 GK-EEAKKCAYTFLVPEQRITGPICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREID 100
                                                                                                                                                                                                                                                                                                                                                   98 DCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 LLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQSVMITLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 EEQCLRIFSRQDTHVSPPLVQVVPQHIPNSQQYTPGLLGGNEIQRDPGYPRDLMPPPDLA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 L-----EKLNLVNMNNIENYV----L-187
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                           47 GKCEEAGECPYQVSLPPLTIQLP-----KQFSRIEEVF--KEVQNLKEIVNSLKKSCQ 97
                                                                                                                                21.2%; Score 505; DB 3; Length 491;
26.9%; Pred. No. 2.2e-38;
.ive 81; Mismatches 137; Indels 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/08960507
Patent No. 6057435
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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                                                                                                                                Query Match 21.2%
Best Local Similarity 26.9%
Matches 131; Conservative
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CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                  101 VLQLVVDVDGN----
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-960-507-4
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 32.4%
Matches 131; Conservative
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                           APPLICATION NUMBER:
FILING DATE: 27-OC
                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 VEMEDWEGNLRYAEYSHFVLGNELNSYRLFLGNYTGNVGNDALQY----HNNTAESTKD 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYY----HQKYRGVRNGIFWGTWPGVSEA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 VRELESEVNKLSSELK--NAKEE---INVLHGRLE-KLNLVNMNNIENYVDSKVANLTFV 183
                                                                                                                                                                                                                                                                                                                                                                                                      184 VNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDP--KNSSFEVY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 CDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILR 301
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08373579
Patent No. 5550490
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                20.6%; Score 489; DB 3; Length 34 36.2%; Pred. No. 3.8e-37; Live 55; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...ureSSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill River Road CITY: Tarrytown STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/373,579
FILING DATE: 17-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
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02-DEC-1994
                       P1130p1
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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----YSLKRVEMKIRPEDFKP 346
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-3216
TELEFAX: 650/25-981
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 HPGGYKSSFKEAKMMIRPKHFKP 439
                                                                                                                                     : 346 amino acids
Amino Acid
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Matches 117; Conservative
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APPLICATION NUMBER: U
FILING DATE: 02-DEC-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                     LENGTH:
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61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 SLL------EHKILEME---GKHKEELDTLKEEKENLQGLVTRQTYIIQELEKQL 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 NLVNMNNIENYVDSKVANLTFVVNSLDGKCSK --- CPSQEQIQSRPVQHLIYKDCSDYYA
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Sequence 4, Application US/08418595

Sequence 4, Application US/08418595

Patent No. 5814464

GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.5%; Score 487; DB 1; Length 497; 32.4%; Pred. No. 1e-36; ive 59; Mismatches 136; Indels
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STREET: 77 old Saw Mill River Road
CITY: Tarrytown
STATE: New York
           FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
us 08/330,261
                                                                                                                                                   REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 86,108
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acids
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RESULT 14
US-08-348-492-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT: NFORMATION:
APPLICATION NUMBER: US 08/319,932
FILING DATE: NFORMATION:
                                                                                                                                                               APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,595
FILING DATE: 06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4, Application US/08665926
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cobert, Robert J. 108
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (914) 345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-418-595-4
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Best Local Similarity
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                                                                                                                        CLASSIFICATION:
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US-08-665,926-4
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162 NLVNMNNIENYVDSKVANLTFVVNSLDGKCSK----CPSQEQIQSRPVQHLIYKDCSDYYA 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 IGKRSSETYRV----TPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 FGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 YNGTAGDALRFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYY 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 LTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLLQQTNEILKIHE-------KN 191
Patent No. 5851797
GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 487; DB 2; Length 49; Pred. No. 1e-36; 59; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 HQ-KYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | ||| | : | | . | | 462 TAGQNHGKLNGIKWHYFKGPS-----YSLRSTTMMIRPLDF 497
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/665,926
                                                                                                                                                                                  Regeneron Pharmaceuticals, Inc.
                                                                                                                                                                                                         777 OÍd Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.5%;
32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (914) 345-2113
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.5%
Best Local Similarity 32.4%
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS: LENGTH: 497 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-665-926-4
                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                 CITY: Tarrytown
                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 10591-6707
                                                                                                                                                                                                         STREET:
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61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
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                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: THE-2 LIGAND, METHOD OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.5%; Score 487; DB 3; Length 49
32.4%; Pred. No. 1e-36;
.ive 59; Mismatches 136; Indels
       395 HQ-KYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRPKHF 437
                                                      462 TAGONHGKLNGIKWHYFKGPS-----YSLRSTTMMIRPLDF 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 GLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION UNDBER:
FILING DATE: 06-APR-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REG 330-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                         Sequence 4, Application US/09162437
Patent No. 6166185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cobert, Robert J. REGISTRATION NUMBER: 36,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: R
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 497 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 32.4'
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-09-162-437-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 GLLLPSTGAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHG------RLEK-L 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLVNMNNIENYVDSKVANLTFVVNSLDGKCSK----CPSQEQIQSRPVQHLIYKDCSDYYA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 YNGTAGDALRENKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYY 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTGTAGKQSSLILH-GAD---FSTKDADNDNCMC-KCALMLTGGWWFDACGPSNLNGMFY 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------KN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
                                               GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: THE-2 LIGAND, METHOD OF MAKING AND USES TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROPERCOPPARMACEULICALS, INC.
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 20.5%; Score 487; DB 2; Length 497; Best Local Similarity 32.4%; Pred. No. 1e-36; Matches 131; Conservative 59; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 LTDVETQVLNQTSRLEIQLLENSLSTYKLEKQLLQQTNEILKIHE---
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/348,492
FILING DATE: 02-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32.143
REFERENCE/DOCKET NUMBER: REG 330B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 347-7000
TELERAX: (914) 347-2113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Sequence 4, Application US/08348492
Patent No. 5879672
                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-348-492-4
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                            CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                           COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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192 SLL------EHKILEME---GKHKEELDTLKEEKENLQGLVTRQTYIIQELEKQL 237
        162 NLVNMNNIENYVDSKVANLTFVVNSLDGKCSK --- CPSQEQIQSRPVQHLIYKDCSDYYA 218
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        οy
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Search completed: February 27, 2001, 12:48:04 Job time: 30 sec

us-09-442-143-2.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 27, 2001, 12:48:09; Search time 19.29 Seconds (without alignments) 734.946 Million cell updates/sec Run on:

US-09-442-143-2 2378 1 MKLANWYWLSSAVLATYGFL......GYKSSFKEAKMMIRPKHFKP 439 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

88757 Total number of hits satisfying chosen parameters: 88757 seqs, 32294092 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	Description			P04469 homo sapien		P02679 homo sapien	_	P12799 bos taurus	P02675 homo sapien		P14480 rattus norv		P19477 parastichop		petromy		rattus	homod	homo	homo	Q29116 sus scrofa	P10039 gallus gall		_		P25805 plasmodium		Q09560 caenorhabdi	P12847 rattus norv	P11055 homo sapien	32	10964	54697	O67032 aquifex aeo
SUMMARIES	ID	FIBX_MOUSE	FIBB_CHICK	FIBH_HUMAN	FIBB_PETMA	FIBG_HUMAN	FIBB_BOVIN	FIBG_BOVIN	FIBB_HUMAN	FIBG_XENLA	FIBB_RAT	FIBA_HUMAN	FIBA_PARPA	FIBA_RAT	FIBG_PETMA	FIBA_CHICK	FIBG_RAT	MFA4_HUMAN	TENX_HUMAN	TENA_HUMAN	TENA_PIG	TENA_CHICK	FIB2_PETMA	SCA_DROME	MFA4_BOVIN	CYSP_PLAFA	NOMR_RAT	YQY1_CAEEL	MYSE_RAT	MYSE_HUMAN	RA18_SCHPO	RPA1_YEAST	MYSJ_DICDI	RF1_AQUAE
	BB:	-	7	П	٦	-	-	-	Н	П	 1	~	7	-		-	-	-	Н	-	-	-	-	_		-	, - 1		-	-		-	-	Н
	Length	432	463	453	477	437	468	444	491	438	479	866	282	782	432	741	445	255	4289	2201	1746	1808	641	774	129	569	485	964	1940	1940	1140	1664	2245	362
% Query	Match	77.9	21.5	20.2	20.2	20.1	19.8	6	σ	g.	g	S)	œ	œ	œ	œ	7	9	16.7	9	9	9	15.1	14.6	7.8	4.8		4.8		٠	4.5	•	4.5	4.4
	Score	1853.5	511.5	481.5	479.5	477.5	471	462	461	456	454.5	451	446	441	428.5	427.5	419	399	397.5	388	386.5	386	358.5	346.5	185.5	115	114.5	114.5	114.5	112		106.5	106	105
Result	No.	1	2	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	

Q49419 mycoplasma Q00496 clostridium									P30995 clostridium
Y328_MYCGE BXE_CLOBO	YP9C_CAEEL KTR6_YEAST	YL17_CAEEL	C9DA_BACTP	CGAO_HELPY	MYS3_HYDAT	TBFG_EPTST	HMW2_MYCGE	ANT1_ONCVO	BXE_CLOBU
		-	-	Н	Н	-	-	Н	٦
756 1250	331 446	1130	1169	1186	539	603	1805	2022	1250
4. 4 4. 4	4 4 4. 4.	4 . 4	4.4	4.4	4.4	4.4	4.4	4.4	4.3
105 105	104.5 104.5	104.5	104.5	104.5	104	104	104	104	103
34 35	36 37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Biochemistry 30:3290-3294(1991).
-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAWMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMEIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
                                                                                                                                                                                                                                                                                      173.
                                                                                                                                                                                                                                                                                                                                                                                                                     360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryoťa; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                Gaps
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an atypical thrombin
                                                                                                                                                                                                                                                                           AE-TAEDSRVQELESQVNKLSSELKNAKDQIQGLQGREETLHLVNMNNIENYVDNKVANL
                                                                                                                                                                                                                                                                                                                                                                                MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVS
                                                                                                                                                                      LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTG
                                                                                                                                                                                                                        YCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL
                                                                                                                                                                                                                                                                                                                                                                                                                     RIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                   KDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANL
                                                                                                                                                                                                                                                                                                               TFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEV
                                                                                                                              7;
                                                                                                       432;
                                                                                                       Length
                      BY SIMILARITY.

BY SIMILARITY.

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2B297F69CCB4A782 CRC64;
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                                                                                                      Score 1853.5; DB 1
Pred. No. 3.4e-119;
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5 (Rel. 34, Last annotation update)
BETA CHAIN PRECURSOR (FRAGMENT).
POTENTIAL.
PROTHROMBINASE.
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19
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01-OCT-1996
FIBRINOGEN BI
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Q02020;
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                        DISULFID
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SEQUENCE
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Best Local
Matches 343
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
SIMILARITY).
SIMILARITY).
SIMILARITY).
SIMILARITY).
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CATALYZES THE EPSILON-(GAMMA-GLUTAMYI)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------LKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVRELE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEVNKLSSELKNAKEEINVLHGRLEKLNLVNANNIENYVDSKVANLTFVVNSLDGKCSKC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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SULFATATION (BY SIMILARITY)
CLEAVAGE (BY THROMBIN; RELE
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INTERCHAIN (WITH ALPHA) (E
INTERCHAIN (WITH ALPHA) (E
INTERCHAIN (WITH ALPHA) (E
INTERCHAIN (WITH GAMMA) (E
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2044CD49BA79EC7B CRC64;
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Blood coagulation; Plasma; Platelet; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71; Mismatches 154;
                                     (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 8.1e-28;
                                                                                                                                                                                                                                                                                                                                           FIBRINOPEPTIDE B)
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HSSP; P02675; 1FZB.
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453 AA;
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HSSP; P02679;
MIM; 134850;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITINE-91369960; PubMed-1892842; Farrel D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.; Farrel D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.; Recombinant human fibrinogen and sulfation of the gamma 'chain."; Biochemistry 30:9414-9420(1991).

-i- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD SPECTOR XIIIA WHICH CATALYZES THE EPSILON-(GAWMA-GLUTAMAL)LYSINE CROSS-LINKING BETWEEN GAWMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. ALTERNATUP PRODUCTS: THIS CHAIN DIFFERS FROM THE GAMMA-A CHAIN AT RESIDUES 434-437 FOLLOWED BY 16 ADDITIONAL RESIDUES OF THE CARBOXYL END. THESE DIFFERENCES ARE PRODUCED BY AN ALTERNATE SPLICING OF THE MRNA IN WHICH THE EIGHTH (LAST) INTRON IS NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: THE GAMMA-B CHAIN IS PRESENT IN ABOUT 10% OF THE FIBRINGEN MOLECULES IN PLASMA BUT ABSENT FROM THOSE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crabtree G.R.;
"Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the 3' end of the gene produces gamma A and gamma B forms of gamma-fibrinogen.";
                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human plasma fibrinogen heterogeneity: evidence for an extended carboxyl-terminal sequence in a normal gamma chain variant
                                                                                                                                                                                                                                                                                                                                       Rixon M.W., Chung D.W., Davie E.W.; "Nucleotide sequence of the gene for the gamma chain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-82068993; PubMed=7306501;
Wolfenstein-Todel C., Mosesson M.W.;
"Carboxy-terminal amino acid sequence of a human fibrinogen
                                                                                                                                                                                                                                                                                                                                                                                                                              CHROMATOGRAPHIC COMPARISON OF GAMMA-A AND GAMMA-B CHAINS.
MEDLINE-81054908; Pubmed-6933547;
Wolfenstein-Todel C., Mosesson M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 285-453 FROM N.A.
MEDLINE-85030379; PubMed-6092346;
Fornace A.J. Jr., Cummings D.E., Comeau C.M., Kant J.A.,
                                                                                                                                                13-AUG-1987 (Rel. 05, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
FIBRINOGEN GAMMA-B CHAIN PRECURSOR (FIBRINOGEN GAMMA').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 77:5069-5073(1980)
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437 GIVWMNWKG-----SWY--SMKKMSMKIKP 459
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                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-85252774; Pubmed-2990550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma-chain variant (gamma').";
Biochemistry 20:6146-6149(1981).
                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 24:2077-2086(1985)
                                                                                        FIBH_HUMAN STANDARD; F P04469; P04470; 21-JUL-1986 (Rel. 01, Created) 13-AUG-1997 (Rel. 05, Last sequol-OCT-1996 (Rel. 34, Last anno
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INTERCHAIN (WITH C-35').
INTERCHAIN (WITH C-34').
INTERCHAIN (WITH C-110 IN BETA).
INTERCHAIN (WITH A-64 IN ALPHA).
INTERCHAIN (WITH C-227 IN BETA).
INTERCHAIN (WITH C-27 IN BETA).
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Blood coagulation; Glycoprotein; Calcium; Platelet; Plasma;
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CROSS-LINK TO 432-LYS AND 4
SULFATATION (PROBABLE).
R -> Y (IN REF. 4).
Y -> R (IN REF. 4).
W; FA647C5E85A2013A CRC64;
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29.3%; Pred. No. 8.7e-26;
ive 59; Mismatches 177;
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EMBL; X02569; AAA52430.1; -
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GOSTRONDHORF-EGNCABODGSGWANNKCHAGHLAGVITGGGTYSASTPRGTDNG 392 AGFRENDNDRAF-EGNCABODGSGWANNKCHAGHLAGVITGGGTYSASTPRGTDNG 392 (TITE 1	THE STANDARD: AM STANDARD: PRT: 477 AA. BB6 (Rel. 12, Last sequence update) 11 11 11 11 11 11 11 11	FT DISHLET	•	FT DISULFI FT DISULFI FT DISULFI	Query Matc	Best Local Matches 1	Oy 29 EI	Db 100 EL	88	Db 127 IN		205		259	. 11 276 DG	Qy 308 NG	DD 336 EG	Oy 359 PD	Db 396 FD	408	Db 456 MN	RESULT 5 FIBG_HUMAN ID FIBG_HU	AC F026/9; DT 21-JUL-	DT 15-JUL-		OC Eukaryo OC Mammali	- 0) <u>2</u> ; <u>p</u>		RL Biochem RN [2]		
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D.W., Chan W.-Y., Davie E.W.;
Cterization of a complementary deoxyribonucleic acid coding for mma chain of human fibrinogen.";
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ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
.ia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                   ch 20.2%; Score 479.5; DB 1; Length 477; 1 Similarity 29.2%; Pred. No. 1.3e-25; 131; Conservative 66; Mismatches 138; Indels 113
                                                                                                                                             B8A95E7E32D09D18 CRC64;
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MEDLINE=98292395; Pubmed=9628725;
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Biochemistry 37:8637-8642(1998).
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                                                                                                                                                                                                                                                                                                                                                                        19 FLSSTCVA-----YVATRDNCCILDERFGSYCPT------TCGIADFLSTYQTK 61
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"Fibrinogen Bern I: substitution gamma 337 Asn-->Lys is responsible for defective fibrin monomer polymerization.";
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Yoshitake S., Okuma M., Ito Y., Takeda Y., Matsuda M.;
"Gene analyses of abnormal fibrinogens with a mutation in the gamma
chain.";
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                                                                                                                                                                         MEDLINE-3022/2007, Ball W.R., Dang C.V.;
Bantia S., Bell W.R., Dang C.V.;
"Polymerization defect of fibrinogen Baltimore III due to a gamma
                                                                                                                                                                                                                                                                                                                                   69;
                                                                                                          Bantia S., Mane S.M., Bell W.R., Dang C.V.; "Fibrinogen Baltimore I: polymerization defect associated with gamma 29201y---vVal (GGC-->GTC) mutation."; Blood 76:2279-2283(1990).
                                                                                                                                                                                                                                                                                                                DB 1; Length 437;
                                                                                                                                                                                                                                                                                                              20.1%; Score 477.5; DB 1; Length 30.8%; Pred. No. 1.5e-25; ive 56; Mismatches 170; Indels
         KYOTO-3 AND OSAKA-2.
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                                                                    int. J. Hematol. 56:129-134(1992).
                    MEDLINE=93043066; PubMed=1421174;
                                                                                       VARIANT BALTIMORE-1.
MEDLINE-91077435; PubMed-2257302;
                                                                                                                                                                       MEDLINE=90227236; PubMed=2328317;
                                                                                                                                                                                                                                          MEDLINE=94003261; PubMed=8400260;
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ID FIBB_BOVIN STANDARD;

AC P02676;

DT 21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                          Blood 82:2104-2108(1993).
                                                                                                                                                                                                                                                                                                                                   Matches 131; Conservative
          VARIANTS ASAHI; KYOTO-1;
                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                           VARIANT BALTIMORE-3
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393 IIWATW 398
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibrinogen.";
Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
-!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [4]
SEQUENCE OF 44-468 FROM N.A.
MEDLINE=81199473; PubMed=6262803;
Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;
"Characterization of a cDNA clone coding for the beta chain of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
ERESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CONVERTED INTO THE HARD CLOT BY FACTON XITIA WHICH CATALYZES THE
EPSILLON-(GAMMA-GLUTAMYLLYSTEN CROSS-LINKING BETWEEN GAMMA CHAINS
(STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & CAMMA), LINKED TO BACH OTHER BY DISULFIDE BONDS.
-!- MISCELLANEOUS: CONVENTSON OF FIRRINGEN TO FIBRIN T TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-79164394; PubMed-434821;
Martinelli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
Hurrell J.G.R., Leach S.J., Scheraga H.A.;
"Amino acid sequences of portions of the alpha and beta chains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasma; Platelet; Glycoprotein; Sulfatation 21 FIBRINOPEPTIDE B.
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INTERCHAIN (WITH ALPHA).
INTERCHAIN (WITH ALPHA).
INTERCHAIN (WITH GAMMA).
INTERCHAIN (WITH ALPHA).
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PYRROLIDONE CARBOXYLIC ACID.
SULFATATION.
                                                                                                                                                                                                                                                                                                                      Blomback B., Doolittle R.F.; ^{\circ} The sequence of amino acids at the N-terminal end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 5-21.
Sjoquist J., Blomback B., Wallen P.;
"Amino acid sequence of bovine fibrinopeptides.";
Ark. Kemi 16:425-436(1960).
                                    annotation update)
         sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                        fibrinopeptide B.";
Acta Chem. Scand. 17:1816-1819(1963).
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01-FEB-1996 (Rel. 33, Last 01-OCT-1996 (Rel. 34, Last FIBRINOGEN BETA CHAIN.
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                                                                                                                                taurus (Bovine).
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                                                                                                                                                Gaps
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Timpl R., Fletzek P.P., Wachter E., van Delden V.;
"Disulfide-linked cyanogen bromide peptides of bovine fibrinogen. I
Isolation and sequence analysis of the chain constituents from the
                                                                                                                                                                                                                                                               -----QNQVQDNENVVNEYSS-------HLEKHQLYIDETVKNNIPTKL
                                                                                                                                                                                                                                                                                                                                                                                                                             291 KYCGVPGEYWLGNDRISQLTNMGPTKLLIEMEDWRGDKVTALLYEGFTVQNEANKYQLSVS
                                                                                                                                                                                                      LCPTGCKLQDTLVRQERPIRKSIEDLRNTVDSVSRTSSSTFQYITLLKNMWKGR-----
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea,
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2DED42F443AA4B37 CRC64;
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                                                                                                                   Length 468
 INTERCHAIN (WITH GAMMA)
                                                                                                                  Score 471; DB 1; L. Pred. No. 4.7e-25; '; Mismatches 149;
               BY SIMILARITY.

BY SIMILARITY..

BY SIMILARITY..

N-LINKED (GLCNAC.
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01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
FIBRINOGEN GAMMA-B CHAIN PRECURSOR (GAMMA').
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30.6%; Pred
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FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                               -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA, 6 GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- MISCELLANGOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA 6 BETA CHAINS, AND THUS EXPOSES FIBRINOPEPTIDES A AND B FROM ALPHA 6 BETA RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HAND CLOT BY FACTOR XIIIA WHICH CATALYZES THE EPSILOW-(GAMMA-GLOTAMYL)LIXSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STROMGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
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BY SIMILARITY.
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INTERCHAIN (WITH C-32').
INTERCHAIN (WITH BETA).
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INTERCHAIN (WITH ALPHA
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PROSITE; PS00514; FIBRIN_AG_C_D
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Best Local Similarity 30.5
Matches 142; Conservative
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76
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PIR; S05313; S05313.
HSSP; P02679; 1FIC.
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---RFNKHY-NHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYH---- 395

LTKSKEM -- ILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNY -NGTAGDAL ----

292

FEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNL-----RREFWLGNDKIHL

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321 GDDSSDKFFTSHNGMQFSTWDSDNDKY-DGNCAEQVGIGWWMNKCHAGHLNGVYYQGGTY 379
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                380 SKTSTPNGYDNGIIWATW------KSRWYSWKKTTWKIIP 413
                                396 --- QKYRGVRNGIFWGTWPGVSEAHPGGYKS---SFKEAKMMIRP 434
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Last annotation update)
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01-JUL-1993 (Rel. 26, Last seque
01-CCT-2D00 (Rel. 40, Last annof
FIBRINOGEN BETA CHAIN PRECURSOR.
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SEQUENCE FROM N.A.
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Asakura S., Shirakawa S.;
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[19]
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REVIEW, AND DISULFIDE BONDS
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X-RAY CRYSTALLOGRAPHY.
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P17634;
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DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILLA.

MISCELLANDROUS: CONVERSION OF FIBRINGEN TO FIRBLY IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPERFIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CATALYZES THE
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                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE. DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXXL
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19.4%; Score 461; DB 1; Length 491;
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Matches 133; Conservative 57; Mismatches 161; Indels 112; Gaps
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"Annormal fibrinogens IJmuiden (B beta Arg14-->Cys) and Nijmegen (B
beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
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                                                                                                                                                                                                                                                           exon 2 of the gene.";
J. Biol. Chem. 260:4390-4396(1985).
-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOME!
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -; NOT_ANNOTATED_CDS.
CAA28674.1; -.
AAA18024.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J00131; AAA98115.1; -.
J00130; AAA98115.1; JOINED.
J00132; AAA98116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA52445.1; -. AAA52445.1; JOINED.
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                                                                                                                                                                      VARIANT NEW YORK-1.
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M26876;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1FZC;
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EMBL;
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TORKVERKAPDA-------GGCLHADPDLGVLCPTGCQLQEALLQQERPIRNSVDELNN 132

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS CALPHA, BETA, 6 GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANGOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIITA WHICH CATALYZES THE EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
                                                                                                                                                                                                     244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGN-------LRREFWLGNDKIHL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bhattacharya A., Shepard A.R., Moser D.R., Holland L.J., "Isolation and characterization of CDNA clones for the gamma subunit of Xenopus fibrinogen, the product of a coordinately regulated gene
                                                 ENVVNEYSSE-------LEKHQLYIDETVNSNIPTNLRVLRSILENLRSKIOK
                                                                                                  194 CPSQEQIQ-----SRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCD
                                                                                                                                              212 LESDVSAQMEYCRTPCTVSCNIPVVSGKECEEIIRKGGETSEMYLIQPDSSVKPYRVYCD
                                                                                                                                                                                                                                  272 MNTENGGWTVIQNRQDGSVDFGRKWDPYKQGFGNVATNTDGKNYCGLPGEYWLGNDKISQ
                                                                                                                                                                                                                                                                                                                                    345 -FNKHYN-HDLKFFTTPDKDNDRY----PSGNCGLYYSSGWWFDACLSANLNGKYY---
134 ESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVANLTFVVNSLDGKCSK
                                                                                                                                                                                                                                                                                                   292 LTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALR-----
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Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90241882; PubMed=2334684;
Pastori R.L., Moskaitis J.E., Smith L.H. Jr., Schoenberg D.R.;
"Estrogen regulation of Xenopus laevis gamma-fibrinogen gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452 YTWDMAKHGTDDGVVWMNWKG-----SWY--SMRKMSMKIRP 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---HOKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRP 434
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10-AUG-1990 (Rel. 15, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
FIBRINOGEN GAMMA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 AA
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                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                   INTERCHAIN (WITH BETA) (BY SIMILARITY).

INTERCHAIN (WITH BETA) (BY SIMILARITY).

INTERCHAIN (WITH BETA) (BY SIMILARITY).

INTERCHAIN (WITH BETA) (BY SIMILARITY).

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BY SIMILARITY.
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INTERCHAIN (WITH C-32') (BY SIMILARITY)
INTERCHAIN (WITH BETA) (BY SIMILARITY)
INTERCHAIN (WITH ALPHA) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                              SSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQVSLPPLTIQLP 69
                                                                                                                                  coagulation; Glycoprotein; Calcium; Plasma; Platelet; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 DGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETM
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the European Bioinformatics Institute. There are no rest
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modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                          158; Indels
                                                                                                                                                      FIBRINOGEN GAMMA CHAIN
                                                                                                                                                                                                                                                                                    19.2%; Score 456; DB 1;
30.4%; Pred. No. 4.5e-24;
tive 69; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                               14 SLALLSSAFGNIIPNTDNCCILDGRFGEYCPT------
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
FIBRINOGEN BETA CHAIN PRECURSOR.
                                                                                                INTERPRO; IPR002181; -. PFAM; PF00147; fibrinogen_C; 1. PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                                                         MW.;
                                                         EMBL; J02894; AAA49709.1; -.
EMBL; M35548; AAA03247.1; -.
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HSSP; P02679; 1FIC.
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-!- FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
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                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89378771; PubMed=2673932;
Bastman E.M., Gilula N.B.;
"Cloning and characterization of a cDNA for the B beta chain of rat fibrinogen: evolutionary conservation of translated and dense of translated sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBGNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANEOUS: CONVERSION OF FIRRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETCHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                    STRAIN=SPRAGUE-DAWLEY; TISSUE-LIVER;
MEDLINE-95143386; PubMed=7841303;
Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.;
"Cloning of the complete coding sequence of rat fibrinogen B beta
chain cDNA: interspecies conservation of fibrin beta 15-42 primary
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-WISTAR; TISSUE-LIVER;
MEDLINE-87134033; PubMed-3817019;
SObcark J., Lotti A.-M., Taroux P., Duguet M.;
Molecular cloning of mRNs sequences transiently induced during
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-26 FROM N.A.
SEQUENCE OF 1-26 FROM N.A.
MEDLINE-84194000; PubMed-6232608;
FOWLKES D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
FOWLKES D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
FOWLKES D.M., Mullis N.T., Semplation of the coordinately expressed fibrinogen genes: homology in the 5' flanking regions.";
Froc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blomback B., Blomback M., Grondahl N.J.;
"Studies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
                                                                                                                                                                                                                                                                                                                                                    structure.";
Blood Coagul. Fibrinolysis 5:487-496(1994).
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SEQUENCE OF 425-479 FROM N.A.
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EMBL; M27220; AAA41160.1; -.
EMBL; K01336; AAA98625.1; -.
EMBL; M35602; AAA41159.1; -.
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norvegicus (Rat).
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PIR; PE0010; PE0010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 NEFLKYRLHVGNYNGTAGDALR -----FNKHYN-HDLKFFTTPDKDNDRY ----PSG 369
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                                                                                                                                                                                                                                                                                                                                                                                                                        167 NNIENYVDSKVANLTFVVNSLDGKCSKCPSQEQIQSR-------PVQHLIYKDCS 214
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                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
LSI -> LS (IN REF. 3).
L -> Q (IN REF. 5).
S -> T (IN REF. 5).
S -> A (IN REF. 5).
R -> K (IN REF. 5).
V -> F (IN REF. 5).
W -> F (IN REF. 5).
W -> F (IN REF. 5).
W -> F (IN REF. 5).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-93090725; PubMed=1457396;
MEDLINE-930807.
MEDLINE-9
                                                                                                                                                                                                                                                                                                                        75;
        INTERCHAIN (WITH THE ALPHA CHAIN)
                                          GAMMA CHAIN)
                                                                                                                                                                                                                                                                                        479;
                                                                                                                                                                                                                                                                                          Length
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                    (BY SIMILARITY).
INTERCHAIN (WITH THE
(BY SIMILARITY).
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Pred. No. 6.4e-24;
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01-0CT-2000 (Rel. 40, Last annotation update)
FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
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N-LINKED
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SEQUENCE FROM N.A. (ALPHA-E FORM)
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                                                                                                                        CARBOHYD
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[5] SEQUENCE OF 1-629 FROM N.A.
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B.F.P.;
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two
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MEDLINE=97472408; PubMed=9333233;
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                                  MEDLINE=76225080; PubMed=936108;
                   VARIANT, AND DISULFIDE BONDS
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Blood 78:149-153(1991).
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- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   476 KEV--TKEVVTS--EDGSDCP-EAMDLGTLSGIGTLDGFRHRHPDEAAFFDTASTGKTFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 IGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 YNGTAGDAL-----RFNKHYNHDLKFFTTPDKDNDRYPSGNCGLYYSSGWWFDACL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   758 YEGTAGDALIEGSVEEGAEYTSHNNMQ---FSTFDRDADQWEE-NCAEVYGGGWWYNNCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 GFFSPMLGEF----VSETESRGSE-SGIFTNTKESSSHHPGIAEFPSRGKSSSYSKQFTS
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impaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94;
"Fibrinogen Lima: a homozygous dysfibrinogen with an A alpha-arginine-141 to serine substitution associated with extra N-Glycosylation at A alpha-asparagine-139. Impaired fibrin gel formation but normal fibrin-facilitated plasminogen activation
                                                                                                                                                                                                                                                                                                                                                                                                                       Arg-->Cys)
and
                                                                                                                                                                                                                                                                                                                                                                  Mosesson P
Soria C.,
                                                                                                                                                                       Hirata H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.0%; Score 451; DB 1; Length 86 32.5%; Pred. No. 2.4e-23; ive 51; Mismatches 137; Indels
                                                                                                                                                                                                                              Asn substitution
characterized by
                                                                                                                                                                                                                                                                                                                                                                Koopman J., Haverkate F., Grimbergen J., Lord S.T.,
Diorio J.P., Siebenlist K.S., Legrand C., Soria J.,
                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular basis for fibrinogen Dusart (A alpha 554 its association with abnormal fibrin polymerization
                                                                                                                                                 MEDLINE-91268018; PubMed-1675636; Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hi Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A., Arcoha-Pinango C.L., Matsuda M.; An A alpha Ser-434 to N-91ycosylated Asn substituti dysfibrinogen, fibrinogen Caracas II, characterized
                                                                          catalyzed by tissue-type plasminogen activator.";
J. Clin. Invest. 90:67-76(1992).
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(Rel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 KEVQNLKEIVNSLKKSCQDCKLQADDNG------
                                                                                                                                                                                                                                                                   fibrin gel formation.";
J. Biol. Chem. 266:11575-11581(1991).
                                                                                                                                                                                                                                                                                                                                              MEDLINE=9323289; PubMed=8473507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                 VARIANT CARACAS-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombophilia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGREGATION
                                                                                                                                                                                                                                                                                                                              DUSART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1991
01-FEB-1991
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P19477;
                                                                                                                                                                                                                                                                                                                                                                                                       Caen J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                            VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386
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                                                                                                                                                                                                                                                                                                         [25]
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          REPETTTTTE BENEVER                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                     "Presence of a vertebrate fibrinogen-like sequence in an echinoderm."; Proc. Natl. Acad. Sci. U.S.A. 87:2097-2101(1990).
-!- SIMILARITY: RELATED TO THE C-TERMINAL PART OF THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 KDCSDYY--AIGKR-SSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                     Stichopodidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 282;
                                                                   Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 LSANLNGKYYHQKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIR 433
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LLSNLNGQYY--DYSGAPS-IYWSYLPGDNDQIP-----FAEMKLRNR 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07326C8865B7D3A2 CRC64;
15-JUL-1999 (Rel. 38, Last annotation update)
FIBRINGEN-LIKE PROTEIN A PRECURSOR (FREP-A).
Barastichopus parvimensis (Sea cucumber).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Elenthuroidea; Aspidochirotacea; Aspidochirotacea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.8%; Score 446; DB 1;
43.2%; Pred. No. 1.2e-23;
tive 33; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        782 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO; IPRODI81; -. PFAM; PFO0147; fibrinogen_C; 1. PROSITE; PSO0514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                 TISSUE-SOFT TISSUES;
MEDLINE-90192754; PubMed-2315305;
Xu X., Doolittle R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1988 (Rel. 06, Created)
01-OCT-1996 (Rel. 34, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32280 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M31326; AAA29962.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A35084; A35084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224
282 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P02671;
                                                                                                        Parastichopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 66
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P06399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            liver regeneration.";
Exp. Cell Res. 169:47-56(1987).
-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PTM: THE ALPHA CHAIN IS NOT GLYCOSYLATED.
-!- MISCELLANEOUS: CONVERSION OF FIRRINGEN TO FIBRIN IS TRIGGERED BY
THROMEIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT THE SOFT CLOT IS
CONVERTED INTO THE HARD CLOT BY FACTOR XIIIA WHICH CATALYZES THE
EPSILON-(GAMMA-GLUTAMYL)IXSINE CROSS-LINKING BETWEEN GAMMA CHAINS
(STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                       "Evolution and structure of the fibrinogen genes. Random insertion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGREGATION.

AGGREGATION.

SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA, 6 GAMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.

CONNECT THE CENTRAL NODULE ARE 2 THREE-CHAIN COLLED COLLS, WHICH
CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE
DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
ALTERNATIVE PROBUCTS: 2 ISOFORMS; ALPHA-E AND ALPHA; ARE
PREDOMINANT FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
INTERCHAIN (WITH BETA) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=WISTAR; TISSUE-LIVER;
MEDLINE-87134033; PubMed-3817019;
Sobczak J., Lotti A.-M., Taroux P., Duguet M.;
"Molecular cloning of mRNA sequences transiently induced during rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO: IPRO02181; -. PFAM; PF00147; fibrinogen_C; 1. PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1. Blood coagulation; Plasma; Platelet; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBRINOGEN ALPHA-E CHAIN.
CLEAVAGE (BY THROMBIN; RELEASE
FIBRINOPEPTIDE A).
                                                                                                                                                                          Crabtree G.R., Comeau C.M., Fowlkes D.M., Fornace A.J. Jr.,
Malley J.D., Kant J.A.;
Fu Y., Cao Y., Hertzberg K., Grieninger G.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBRINOPEPTIDE A.
                                                                                                                                                                                                                                                                                                                                                                                                              Blomback B., Blomback M., Grondahl N.J.;
"Studies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 458-550 FROM N.A. (ALPHA FORM).
                                                                                                                                       MEDLINE=86011580; PubMed=4046033;
                                                                                                       (ALPHA FORM)
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                                                                                                                                                                                                                                                                                                              J. Mol. Biol. 185:1-19(1985)
                                                                                                                                                                                                                                                                              introns or selective loss?";
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782
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56
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 20-36
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                                                                   [2]
SEQUENCE FROM
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A B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDRYPSGNCGLYYSSGWWFDACLSANLNGKYY------HQKYRGVRNGIFWGTWPGV 413
                                                                                                                                                                                                                                                                 125 VGDNRVRELESEVNKLSSELKNAKE--EINVLH---GRLEKLNLVNMNNIENYVDSKVAN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                             253 VLQARLDGSTNFTRTWQDYKAGFGNL----RREFWLGNDKIHLLTKSKEMILRIDLEDFN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   707
                                                                                                                                                                                                                                       Gaps
             (BY SIMILARITY).
INTERCHAIN (WITH BETA) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                             530 QEGDTRTTKRGRARTMRDCDDVLQTHPSGAQNGIFSIKLPGSSKIFSVYCDQETSLGGWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKEAYAEY-HFRVGSEAEGYALQVSSYQGTAGDALMEGSVEEGTEYTSHSNMQFSTFDRD
                                                                                                                                                                                                                                                                                                                                                                                      -----PKNSS-FEVXCDMETMGGGWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 GVELYALYDQFYVANEFLKYRLHVGNYNGTAGDAL-----RFNKHYNHDLKFFTTPDKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                       86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strong D.D., Moore M., Cottrell B.A., Bohonus V.L., Pontes M., Evans B., Riley M., Doolittle R.F.; "Lamprey fibrinogen gamma chain: cloning, cDNA sequencing, and
                                      BY SIMILARITY.

DCDD -> GIHA (IN ISOFORM ALPHA).

MISSING (IN ISOFORM ALPHA).

G -> DEGAG (IN REF. 3).

Q -> E (IN REF. 2).

D -> E (IN REF. 2).

ASRGDLP -> LREEIYQ (IN REF. 2).
                                                                                                                                                                                                                                                                                                                          LIFVVNSLDGKCSKCPSQEQIQSRPVQHL-IYKDCSDYYAIGKRSSETYRVTPD---
INTERCHAIN (WITH C-165 IN GAMMA)
                                                                                                                                                                                                        DB 1; Length 782;
                                                                                                                                                                                                       18.5%; Score 441; DB 1; Length 78
31.0%; Pred. No. 1e-22;
tive 61; Mismatches 116; Indels
                                                                                                                              ASRGDLP -> LREEIYQ (IN REF
S -> K (IN REF. 4).
744834DAE76D34C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
FIBRINOGEN GAMMA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-----YSLWAVRMKIRP 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414 SEAHPGGYKSSFKEAKMMIRP 434
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E
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Biochemistry 24:92-101(1985).
                                                                                                                                                               86685
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                    140
212
276
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                                                                                                                                                                                                                   Local Similarity
les 118; Conserv
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547
551
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1140
212
181
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                                          DISULFID
VARSPLIC
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CONFLICT
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CONFLICT
DISULFID
                            DISULFID
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT IS CONVERTED INTO THE HABD CLOT BY FOATON XIIIA WHICH CATALYZES THE EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 RLQQQLVDIRQTCSR--SCQDTTANKISPITGKDCQQVVDNGGKDSGLYYIKPLKAKQPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFG----NLRREFWLGNDKIHLLTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                    Blood coagulation; Plasma; Glycoprotein; Signal.
SIGNAL
SIGNAL
1 24 BY SIMILARITY.
CHAIN 25 432 FIBRINOGEN GAMMA CHAIN.
DISULFID 32 32 INTERCHAIN (WITH THE GAMMA CHAIN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN (WITH THE BETA CHAIN) (BY SIMILARITY).
INTERCHAIN (WITH THE ALPHA CHAIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAMMA CHAIN)
                                                         (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH THE BETA (BY SIMILARITY). INTERCHAIN (WITH THE GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINKED (GLCNAC. . .).
B503979B296DFB24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 3.3e-22; 46; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RNGIFWGTWPGVSEAHPGGYKSSFKEAKMMIRP 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.0%; Score 428.5; Best Local Similarity 33.8%; Pred. No. 3.3 Matches 114; Conservative 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY
                                                                                                                                                                                                                                                         INTERPRO; IPR002181; -. PFAM: PF00147; fibrinogen_C; 1. PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MM;
                                                                                                                                                                                                        EMBL; K03049; AAA49262.1; -.
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348
227
432 AA;
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P14448;
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                                                                                                    This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBRINOPEPTIDE A.
FIBRINGGEN ALPHA-E CHAIN.
PYRROLIDONE CARBOXYLIC ACID.
INTERCHAIN (WITH C-42') (BY SIMILARITY).
(BY SIMILARITY).
INTERCHAIN (WITH THE BETA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH THE GAMMA CHAIN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMEIN, WHICH CLEAVES FIBRINOPETIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-E AND ALPHA, ARE PRODUCED BY ALTERNATIVE SPLICING. THE ALPHA FORM IS THE PREDOMINANT FORM.
                                                                                                                                                                                                                                   SEQUENCE OF 5-741 FROM N.A.
MEDLINE=90311369; PubMed=2367530;
Weissbach L., Grieninger G.;
"Bipartite mRNA for chicken alpha-fibrinogen potentially encodes amino acid sequence homologous to beta- and gamma-fibrinogens.";
Proc. Natl. Acad. Sci. U.S.A. 87:5198-5202(1990).
                                                                                                                                                                                                     Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blood coagulation; Plasma; Signal; Alternative splicing
        01-JAN-1990 (Rel. 13, Created)
01-007-1996 (Rel. 34, Last sequence update)
10-DEC-1998 (Rel. 37, Last annotation update)
FIBRINOGEN, ALPHA/ALPHA-E CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO, IPR002181; -.
PFAM; PF00147; fibrinogen_C; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMEL, U20799, AAB60686.1; JOINED. EMEL, U20801, AAB60686.1; JOINED. EMEL, U20801, AAB60686.1; JOINED. EMEL, U20802, AAB60686.1; JOINED. EMEL, U20803; AAB60685.1; JOINED. EMEL, U20800, AAB60685.1; JOINED. EMEL, U20800, AAB60685.1; JOINED. EMEL, U20801, AAB60685.1; JOINED. EMEL, W34096, AAA99306.1; JOINED. EMEL, M34096, AAA99306.1; JOINED. EMEL, M34096, AAA99306.1; JOINED. EMEL, M34096, AAA99307.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U20803; AAB60686.1; -
                                                                                                                                                                         SEQUENCE OF 1-4 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
33
741
19
46
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DISULFID
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                                                                                                                                         Gallus.
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	11;	
	tch 18.0%; Score 427.5; DB 1; Length 741; al Similarity 39.2%; Pred. No. 7.8e-22; 96; Conservative 39; Mismatches 77; Indels 33; Gaps KDCSDYYAIGKRSSETYRVTPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRT 267	WQDYRAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVAN 323 #QDYRAGFGSVLGARLALGNENIHLLTGN-DTLLRVELEDWDGNAAYAEY IVQVGT 621 #QDYRRGFGSVDGKGQGELWLGNENIHLLTQN-DTLLRVELEDWDGNAAYAEY IVQVGT 621 EFLKYRLHVGNYNGTAGDALRPNKHYNHDLKFFTTPDKDNDRYPSGNCGLYSS 377 #QDYRAGFGAGDALRPNKHYNHDLKFFTTPDKDNDRYPSGNCGLYSS 377 #ALTVSSYEGTAGDALVAGWLEEGSEYTSHQMQFTFDRDQHWEE-SCAEVYGG 680 GWWFDACLSANLNGKYYQKYRGFTFRAQMQFTFBRDQHWEE-SCAEVYGG 680 #WFDACLSANLNGKYYQKYRGFTFRAQMQFTFBRDGYRSSFKEAK 429 #HIII
	82438 18.09 39.29 vative KRSSETYF : : :	RRE : : GGGGE GTAGD GTAGD GKYY-
68 180 184 310 333 506 510	SEQUENCE 741 AA; Query Match Best Local Similarity Matches 96; Conserv 211 KDCSDYYALGK : 505 KDCDDIRQKHTSGA	WODYKAGFCNLRREFWLG : : : WODYRRGFGSVDGGGELWLG BFLKYRLHVGNYNGTAGDAL BFLKYRLHVGNYNGTAGDAL BFGYALTVSYFGTAGDALV SWWFDACLSANLNGKYYHC SWWFDACLSANLNGKYYHC SWWFDACLSANLNGKYYHC SWWYNSCQAANLNGTYYPGGHY MIRP 434
LFID LFID LFID LFID LFID LFID LFID	ry Match t Local S ches 96 211 KDCS 211 KDCS	
DISULFID DISULFID DISULFID SITE VARSPLIC	SEQUENCE Query Match Best Local Matches 9 211 KDC 505 KDC	268 564 324 622 378 681 430 733
	SQ Que Bes Mat Qy Db	0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0

Search completed: February 27, 2001, 12:52:02 Job time: 233 sec